

FIGURE 1

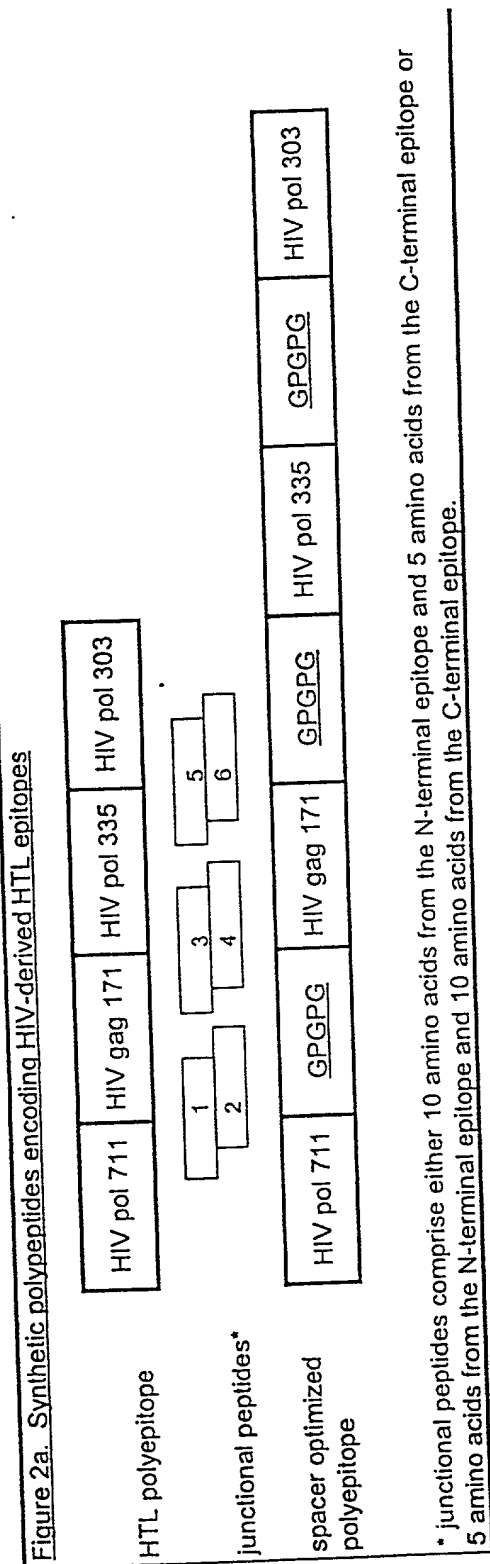
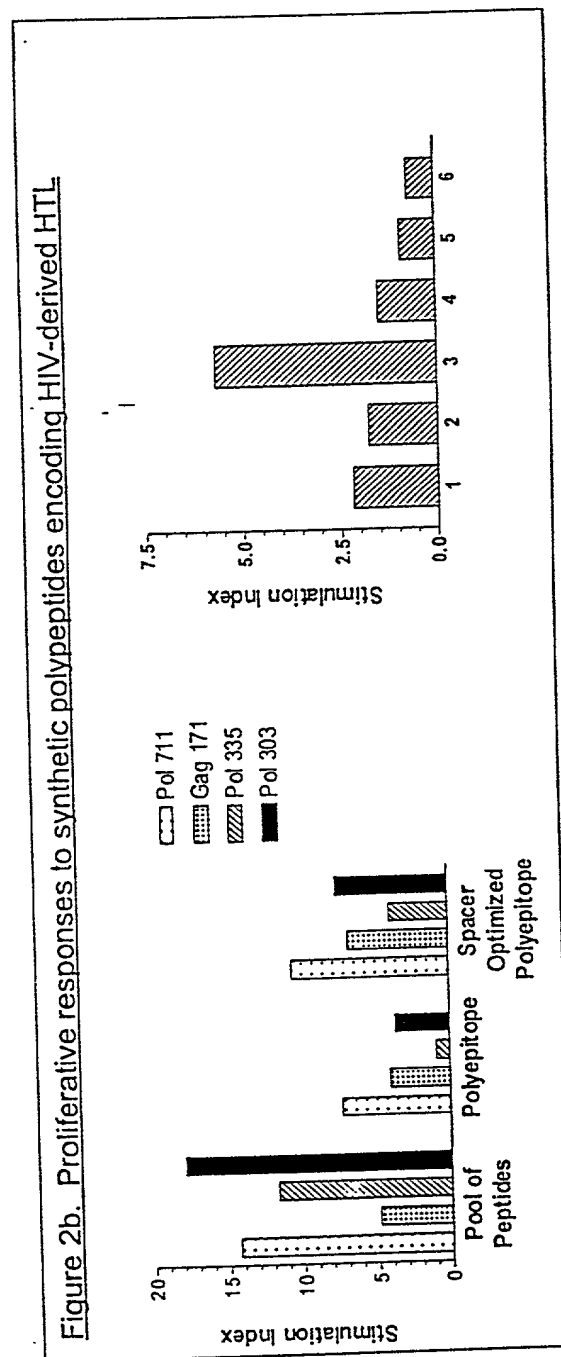
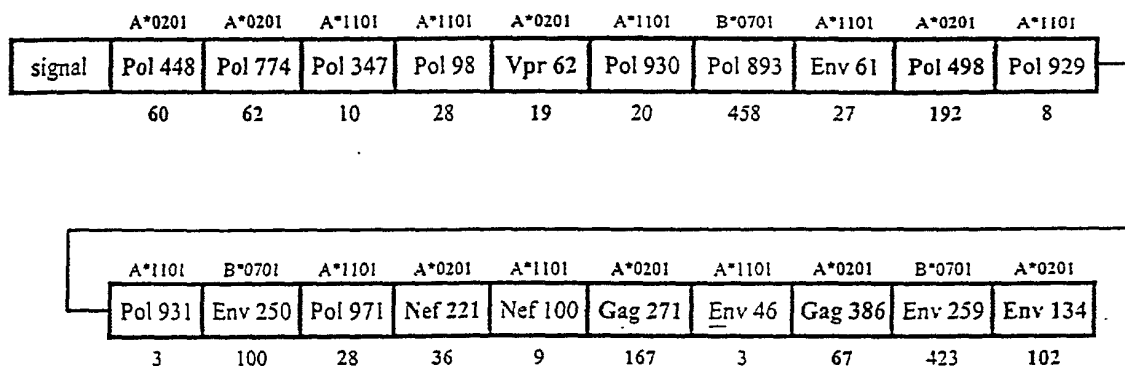


FIGURE 2

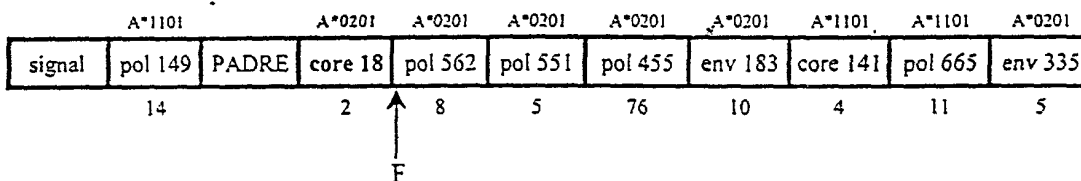


a: HIV-FT

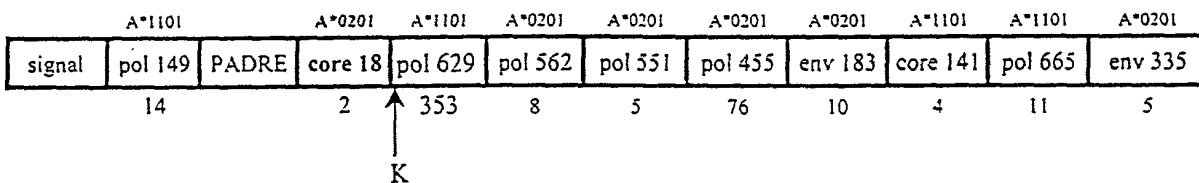


b: HBV-specific multiepitope constructs

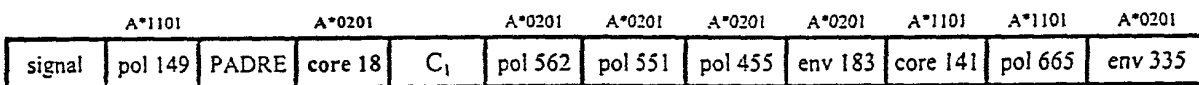
HBV.1



HBV.2

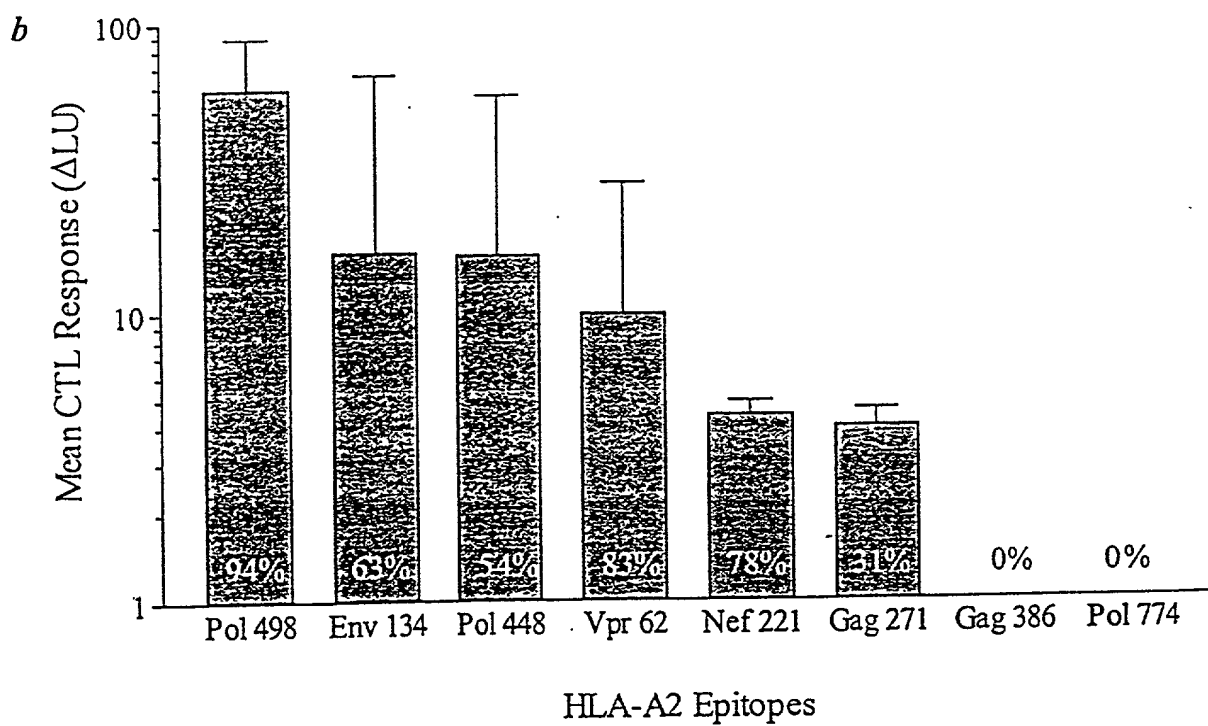
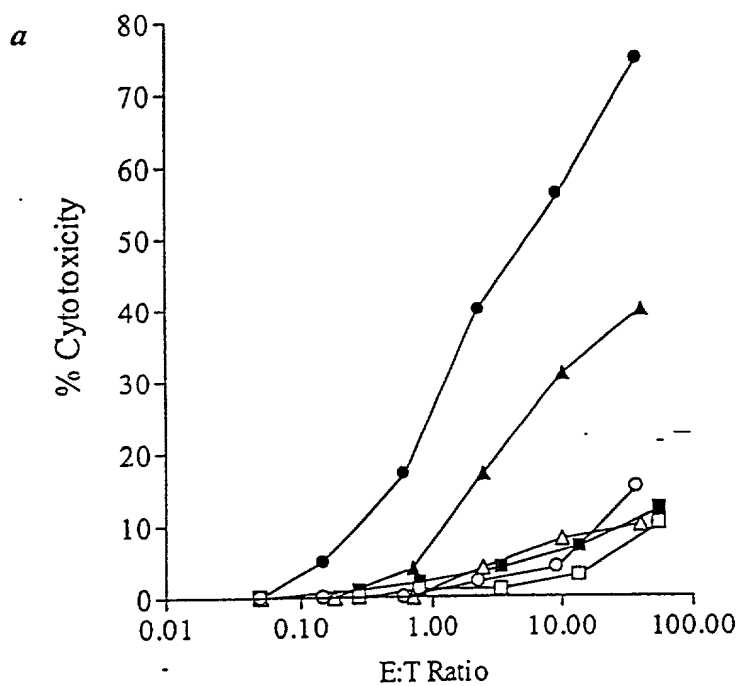


HBV.1X



C<sub>1</sub>= either W, Y, L, K, R, C, N or G

FIGURE 3



**FIGURE 4**

TOC390"8T046860

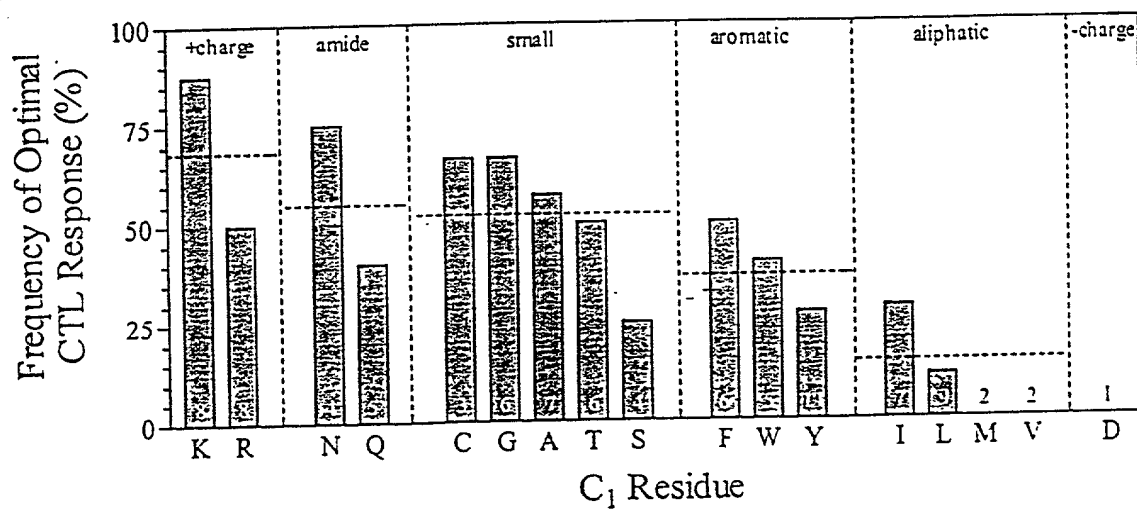
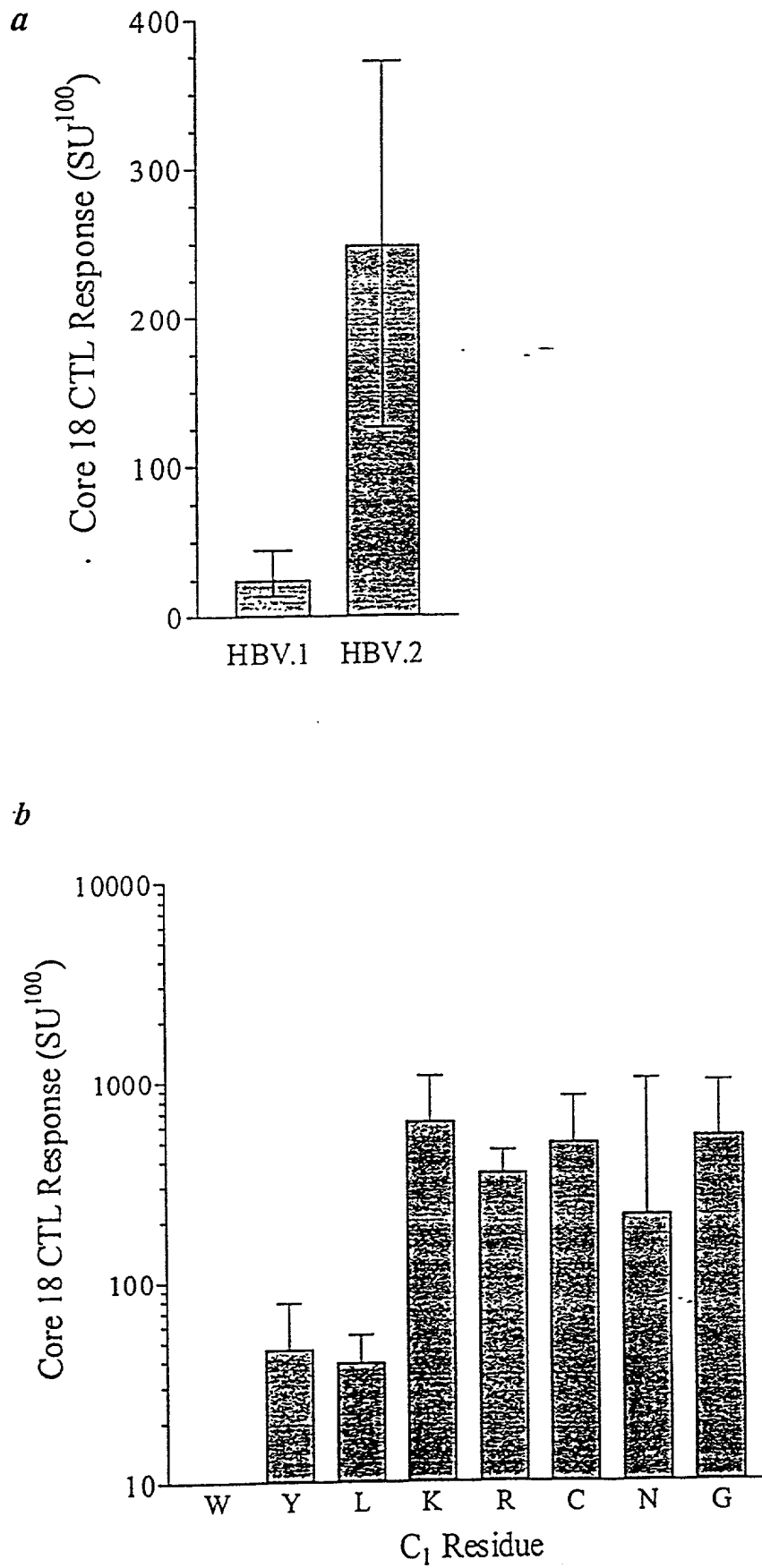


FIGURE 5

FIGURE 6



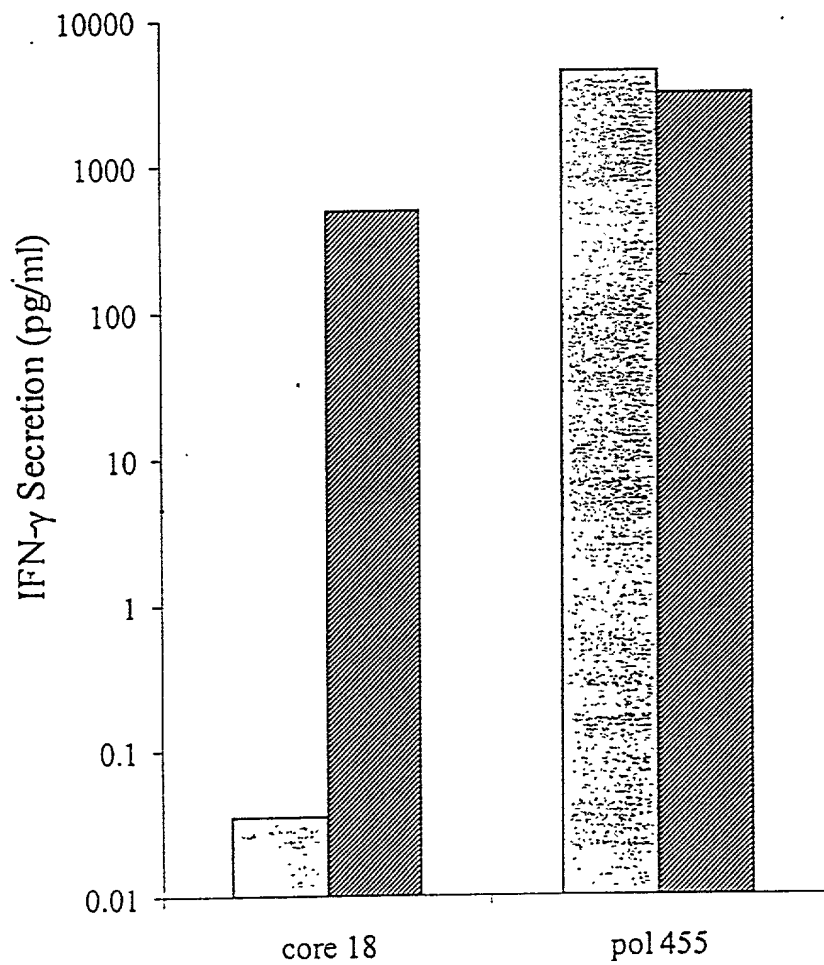


FIGURE 7

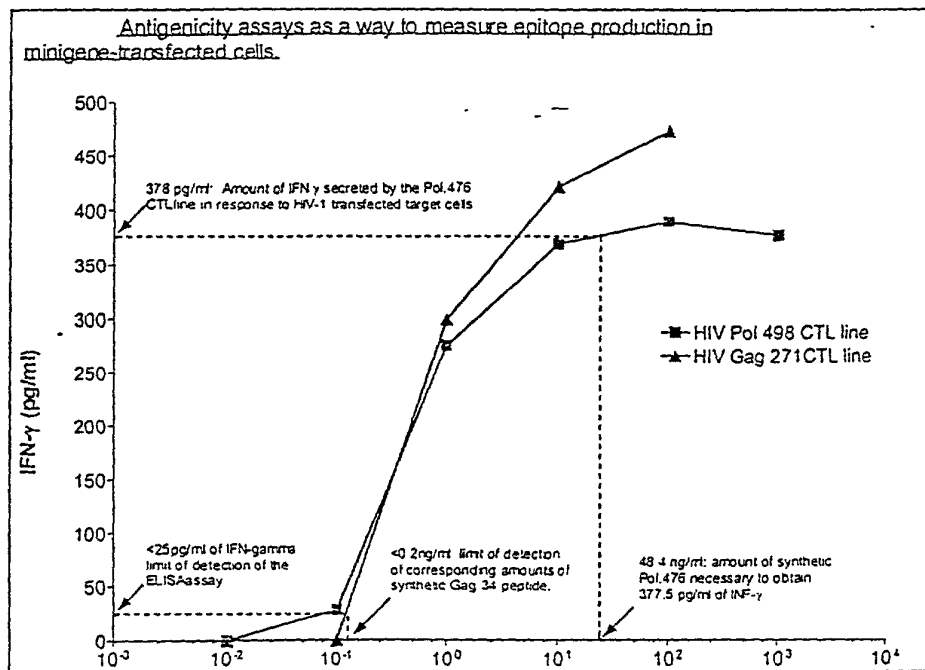


FIGURE 8



EP-HIV-1090

signal	pol 448	gag	env 250	env 259	PADRE	nef 94	env 134	gag 386	pol 722	pol 347	env 61
A*0201	A*0201	B*0701	B*0701	A*1101	A*0201	A*0201	A*0201	A*0201	A*0201	A*1101	A*1101

Pol 893	gag 237	env 47	pol 929	gag 545	nef 221	vpr 62	pol 971	pol 98	rev 75	gag 271
B*0701	A*1101	A*1101	B*0701	A*0201	A*0201	A*1101	A*1101	B*0701	A*0201	A*0201

HIV-CPT

signal	env 259	pol 971	pol 98	PADRE	rev 75	pol 347	env 134	pol 929	pol 722	pol 893	pol 498
B*0701	A*1101	A*1101	B*0701	A*1101	A*0201	A*1101	A*1101	A*1101	A*1101	B*0701	A*0201

nef 221	gag 386	vpr 62	env 250	env 47	gag 237	gag 545	env 61	pol 448	nef 94	gag 271
A*0201	A*0201	B*0701	A*1101	B*0701	A*1101	A*0201	A*1101	A*0201	B*0701	A*0201

HIV-TC

signal	Pol 597	Pol 347	Pol 722	Env 250	Gag 237	NeF 221	Pol 132	Gag 317	Env 61	Gag 162
A*2402	A*1101	A*1101	B*0701	B*0701	A*0201	A*0201	A*0201	A*0201	A*1101	A*1101

Pol 448	Vpr 46	NeF 100	Pol 295	Env 671	Pol 183	Gag 271	Pol 244	Rev 75	Pol 893	Env 651
A*0201	A*2402	A*1101	A*0201	A*0201	A*0201	A*0201	A*2402	B*0701	B*0701	A*0201

Pol 498	Pol 186	Env 55	Pol 98	Pol 533	Gag 386	Pol 163	Pol 684	Env 259	Pol 368	Pol 929
A*0201	B*0701	A*2402	A*1101	A*0201	A*0201	A*0201	A*0201	A*0201	A*0201	A*1101

Pol 530	Vpr 14	Pol 971	NeF 94	Env 681	Vif 7	Pol 579	PADRE	Env 134	Pol 774	Env 163
A*2402	A*2402	A*1101	B*0701	A*0201	A*1101	A*0201	A*0201	A*0201	A*0201	A*0201

Env 47	Vpr 59	Pol 772	Gag 545
A*1101	A*0201	B*0701	B*0701

FIGURE 9

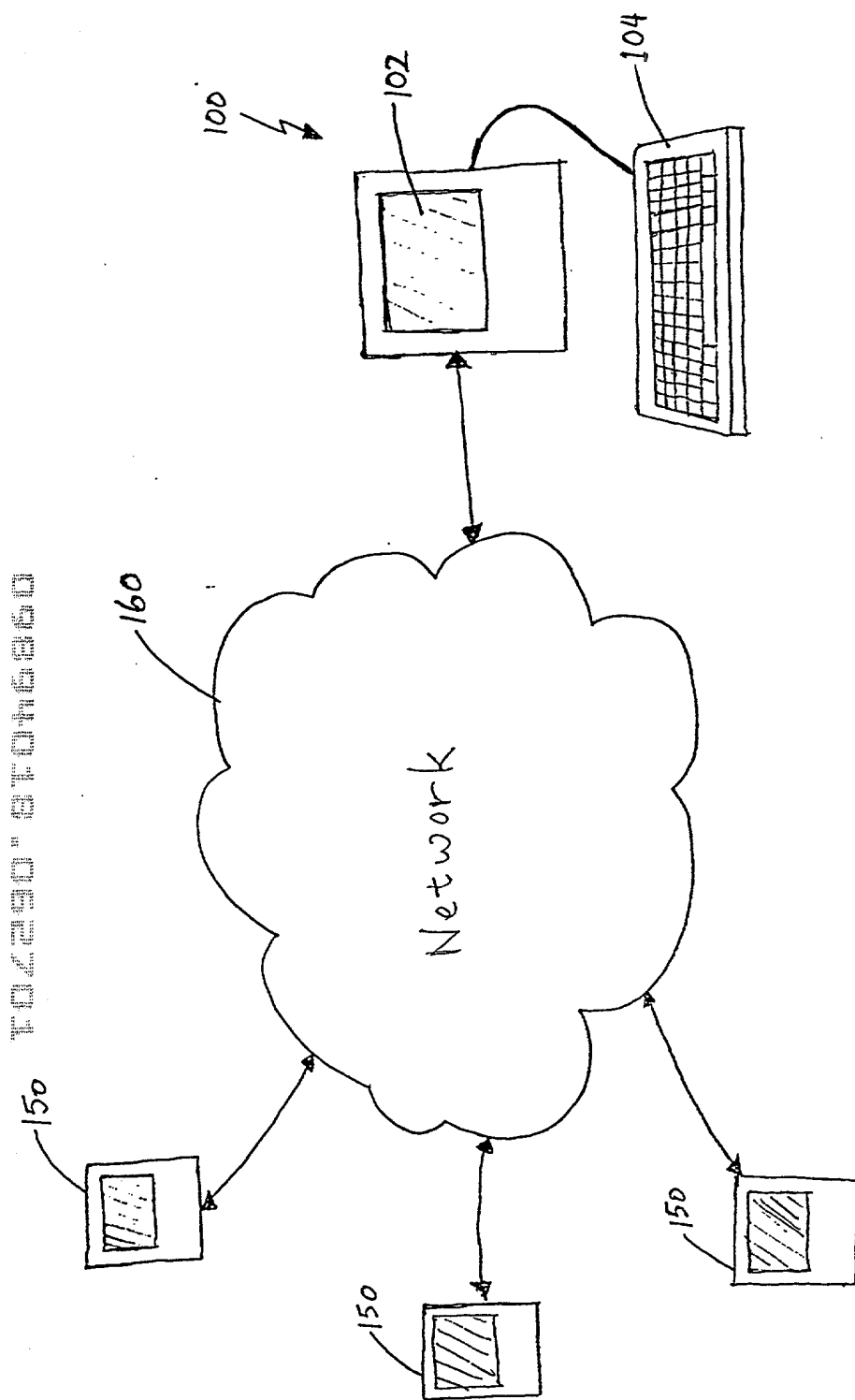


FIGURE 10

200  
⚡

Sequence	Length	Code
VLAEAMSQV	9	A
ILKEPVHGV	9	B
TLNFPISPI	9	C
SLLNATDIAV	10	D
QMAVFIHNFK	10	E
VTVYYGVVPWK	11	F
FPVRPQVPL	9	G
YPLASLRSLF	10	H
VITYQYMDDLV	10	I
IYQEPFKNL	9	J
IWGCSGKLI	9	K

202

AA	C+1 ranking	N-1 ranking
K	2.20	0.64
C	2.00	1.00
N	2.00	0.00
G	1.80	1.33
T	1.50	0.00
A	1.33	1.21
F	1.33	1.00
S	1.33	0.00
W	1.20	0.00
Q	1.20	0.00
R	1.17	1.57
M	1.00	0.00
Y	1.00	0.75
I	0.86	0.50
L	0.75	2.20
V	0.00	1.19
D	0.00	0.00
H	0.00	0.00
E	0.00	0.00
P	0.00	0.00

204

#### Motif Specification

XXXX(FY)XX(LIMV)  
 XXXX(FY)XXX(LIMV)  
 XXXXNXXX(LIMV)  
 XXXXNXXXX(LIMV)  
 X(LM)XXXXXXV  
 X(LM)XXXXXXXV  
 X(LMVT)XXXXXX(KRY)  
 X(LMVT)XXXXXXX(KRY)  
 XPXXXXXX(LIMVF)  
 XPXXXXXXX(LIMVF)

206

FIGURE 11A

MaxInsertions={enter value here} 208  
OutputToScreen=yes/no 210  
OutputToFile=yes/no 212  
MinimumAccepted={enter value here} 214  
MaxDuplicateFunctionValues={enter value here} 216  
MaxSearchTime (min.)={enter value here} 218  
Exhaustive=yes/no 220  
NumStochasticProbes={enter value here} 222  
MaxHitsPerProbe={enter value here} 224  
RandomProbeStart=yes/no 226

**FIGURE 11B**

090403-0001  
T02300-01040300

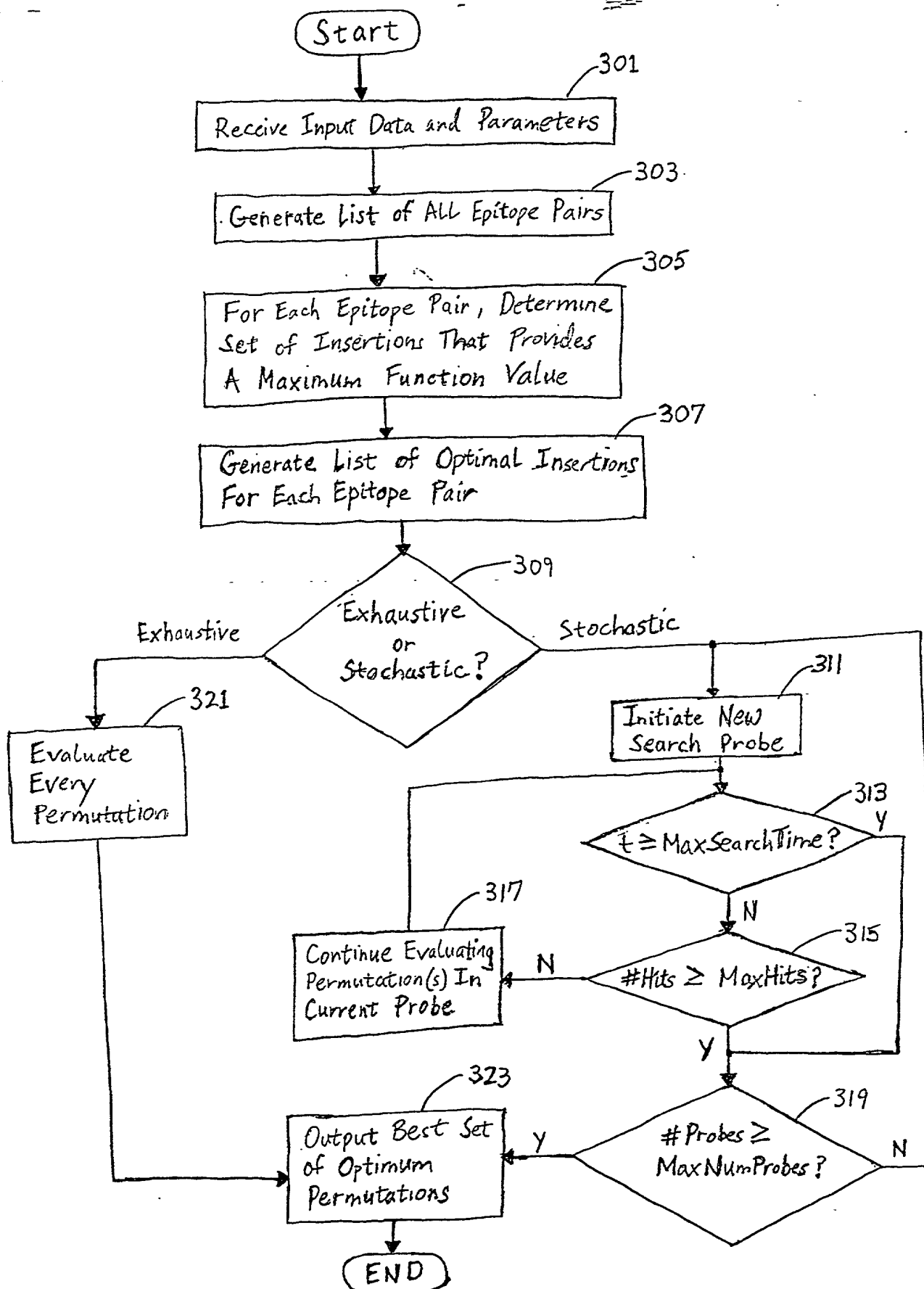


FIGURE 12

Junctional Analyzer run on Saturday, February 26, 2000 09:06:23 pm.

The following non-zero AA weights will be used.

AA	N-1 ranking	C+1 ranking
A	1.21	1.33
C	1.00	2.00
F	1.00	1.33
G	1.33	1.80
I	0.50	0.86
K	0.64	2.20
L	2.20	0.75
M	0.00	1.00
N	0.00	2.00
Q	0.00	1.20
R	1.57	1.17
S	0.00	1.33
T	0.00	1.50
V	1.19	0.00
W	0.00	1.20
Y	0.75	1.00

204

The following 10 motif specifications will be used to search for junctionals.

Count	Motif Specification
1	XXXX(FY)XX(LIMV)
2	XXXX(FY)XXX(LIMV)
3	XXXXNXXX(LIMV)
4	XXXXNXXXX(LIMV)
5	X(LM)XXXXXXV
6	X(LM)XXXXXXXV
7	X(LMVT)XXXXXX(KRY)
8	X(LMVT)XXXXXX(KRY)
9	XPXXXXXX(LIMVF)
10	XPXXXXXX(LIMVF)

206

Code	Peptide	Length
A	VLAAMSQV	9
B	ILKEPVHGV	9
C	TLNFPISPI	9
D	SLLNATDIAV	10
E	QMAVFIHNFK	10
F	VTVYYGVPVWK	11
G	FPVRPQVPL	9
H	YPLASLRS LF	10
I	VIYQYMDDL Y	10
J	IYQEPFKNL	9
K	IWGCSGKLI	9

202

MaxInsertions = 4 (208)

FIGURE 13A

OutputToScreen = No

OutputToFile = Yes

MinimumValueAccepted = 0

MaxDuplicateFunctionValues = 50

SearchTime = 5

NumStochasticProbes = 10

MaxHitsPerProbe = 25

RandomProbeStart = Yes

Col. 1 Code 1	Col. 2 I1	Col. 3 I2	Col. 4 I3	Col. 5 I4	Col. 6 Code 2	Col. 7 C	Col. 8 N	Col. 9 C+N	Col. 10 J	Col. 11 MaxFunc.
A	C	A		L	B	2.00	2.20	4.40	0	8.80
A	C			L	C	2.00	2.20	4.40	0	8.80
A	C			L	D	2.00	2.20	4.40	0	8.80
A	C			L	E	2.00	2.20	4.40	0	8.80
A	C			R	F	2.00	1.57	3.14	2	1.57
A	C			R	G	2.00	1.57	3.14	1	3.14
A	C			R	H	2.00	1.57	3.14	0	6.28
A	G				I	1.80	1.33	2.39	1	2.39
A	C	A	A	G	J	2.00	1.33	2.66	0	5.32
A	C			R	K	2.00	1.57	3.14	0	6.28
B	C	A	A	G	A	2.00	1.33	2.66	0	5.32
B	C	A		R	C	2.00	1.57	3.14	0	6.28
B	C	A		R	D	2.00	1.57	3.14	0	6.28
B	C	A		R	E	2.00	1.57	3.14	0	6.28
B	C	A	A	G	F	2.00	1.33	2.66	1	2.66
B	C			R	G	2.00	1.57	3.14	1	3.14
B	C			R	H	2.00	1.57	3.14	0	6.28
B	C	A	A	G	I	2.00	1.33	2.66	1	2.66
B	C	A	A	G	J	2.00	1.33	2.66	0	5.32
B	C	A	A	G	K	2.00	1.33	2.66	0	5.32
C	C	A		R	A	2.00	1.57	3.14	1	3.14
C	C	A		R	B	2.00	1.57	3.14	1	3.14
C	C			L	D	2.00	2.20	4.40	1	4.40
C	C	A		R	E	2.00	1.57	3.14	1	3.14
C	C			R	F	2.00	1.57	3.14	1	3.14
C	C			R	G	2.00	1.57	3.14	1	3.14
C	C			R	H	2.00	1.57	3.14	0	6.28
C	C	A		R	I	2.00	1.57	3.14	1	3.14
C	C	A	A	R	J	2.00	1.57	3.14	0	6.28
C	C	A	A	R	K	2.00	1.57	3.14	0	6.28

FIGURE 13B

09854013-062701

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
D	C			L	A	2.00	2.20	4.40	0	8.80
D	C			L	B	2.00	2.20	4.40	0	8.80
D	C			L	C	2.00	2.20	4.40	0	8.80
D	C			L	E	2.00	2.20	4.40	0	8.80
D	G				F	1.80	1.33	2.39	0	4.79
D	C			R	G	2.00	1.57	3.14	0	6.28
D	C	A	A	G	H	2.00	1.33	2.66	0	5.32
D	C			L	I	2.00	2.20	4.40	1	4.40
D	C	A		G	J	2.00	1.33	2.66	0	5.32
D	C			R	K	2.00	1.57	3.14	0	6.28
E	C	A	A	L	A	2.00	2.20	4.40	0	8.80
E	C	A	A	L	B	2.00	2.20	4.40	0	8.80
E	C	A	A	L	C	2.00	2.20	4.40	0	8.80
E	C	A	A	L	D	2.00	2.20	4.40	0	8.80
E	C	A		R	F	2.00	1.57	3.14	0	6.28
E	C	A		R	G	2.00	1.57	3.14	0	6.28
E	C	A		R	H	2.00	1.57	3.14	0	6.28
E	C	A	A	L	I	2.00	2.20	4.40	0	8.80
E	C	A		R	J	2.00	1.57	3.14	0	6.28
E	C	A		R	K	2.00	1.57	3.14	0	6.28
F	K	A	A	L	A	2.20	2.20	4.84	1	4.84
F	K	A	A	G	B	2.20	1.33	2.93	1	2.93
F	K	A	A	G	C	2.20	1.33	2.93	0	5.85
F	K	A	A	G	D	2.20	1.33	2.93	0	5.85
F	K	A		G	E	2.20	1.33	2.93	0	5.85
F	K	A		G	G	2.20	1.33	2.93	1	2.93
F	K	A		G	H	2.20	1.33	2.93	1	2.93
F	K	A	A	G	I	2.20	1.33	2.93	1	2.93
F	K			R	J	2.20	1.57	3.45	1	3.45
F	K			R	K	2.20	1.57	3.45	0	6.91
G	C	A		R	A	2.00	1.57	3.14	1	3.14
G	C	A		R	B	2.00	1.57	3.14	2	1.57
G	C			R	C	2.00	1.57	3.14	1	3.14
G	C	A		L	D	2.00	2.20	4.40	1	4.40
G	C			R	E	2.00	1.57	3.14	2	1.57
G	C			L	F	2.00	2.20	4.40	4	1.10
G	C			G	H	2.00	1.33	2.66	0	5.32
G	C	A	A	R	I	2.00	1.57	3.14	2	1.57
G	C	A	A	R	J	2.00	1.57	3.14	1	3.14
G	C	A	A	R	K	2.00	1.57	3.14	0	6.28
H	C	A	A	G	A	2.00	1.33	2.66	0	5.32
H	C	A	A	G	B	2.00	1.33	2.66	1	2.66
H	C	A		G	C	2.00	1.33	2.66	0	5.32
H	C	A		G	D	2.00	1.33	2.66	0	5.32
H	C	A	A	G	E	2.00	1.33	2.66	0	5.32
H	C	A	A	G	F	2.00	1.33	2.66	1	2.66
H	C			R	G	2.00	1.57	3.14	1	3.14
H	C	A	A	G	I	2.00	1.33	2.66	1	2.66
H	C	A	A	G	J	2.00	1.33	2.66	1	2.66
H	C	A	A	G	K	2.00	1.33	2.66	0	5.32

FIGURE 13C



Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
I	K	A	A	G	A	2.20	1.33	2.93	0	5.85
I	K	A	A	G	B	2.20	1.33	2.93	1	2.93
I	K	A		G	C	2.20	1.33	2.93	0	5.85
I	K	A		G	D	2.20	1.33	2.93	0	5.85
I	K	A	A	G	E	2.20	1.33	2.93	0	5.85
I	K	A	A	G	F	2.20	1.33	2.93	1	2.93
I	K	A		R	G	2.20	1.57	3.45	1	3.45
I	K	A	A	G	H	2.20	1.33	2.93	0	5.85
I	K	A	A	G	J	2.20	1.33	2.93	1	2.93
I	K	A	A	G	K	2.20	1.33	2.93	0	5.85
J	K	A	A	R	A	2.20	1.57	3.45	0	6.91
J	K	A	A	R	B	2.20	1.57	3.45	1	3.45
J	K	A		R	C	2.20	1.57	3.45	0	6.91
J	K	A		R	D	2.20	1.57	3.45	0	6.91
J	K	A		R	E	2.20	1.57	3.45	1	3.45
J	K	A	A	R	F	2.20	1.57	3.45	2	1.73
J	K			R	G	2.20	1.57	3.45	1	3.45
J	K			R	H	2.20	1.57	3.45	0	6.91
J	K	A	A	R	I	2.20	1.57	3.45	1	3.45
J	K	A	A	R	K	2.20	1.57	3.45	0	6.91
K	K			L	A	2.20	2.20	4.84	0	9.68
K	K			L	B	2.20	2.20	4.84	0	9.68
K	K			L	C	2.20	2.20	4.84	0	9.68
K	K			L	D	2.20	2.20	4.84	0	9.68
K	K	A	A	L	E	2.20	2.20	4.84	0	9.68
K	K	A	A	R	F	2.20	1.57	3.45	1	3.45
K	G				G	1.80	1.33	2.39	0	4.79
K	K			R	H	2.20	1.57	3.45	0	6.91
K	K			L	I	2.20	2.20	4.84	1	4.84
K	K			R	J	2.20	1.57	3.45	0	6.91

Junctional Analyzer took 142.77 seconds.

FIGURE 13D

102250" 87045850

Figure 3a: CTL responses induced by EP HIV-1090 relative to individual peptides in IFA

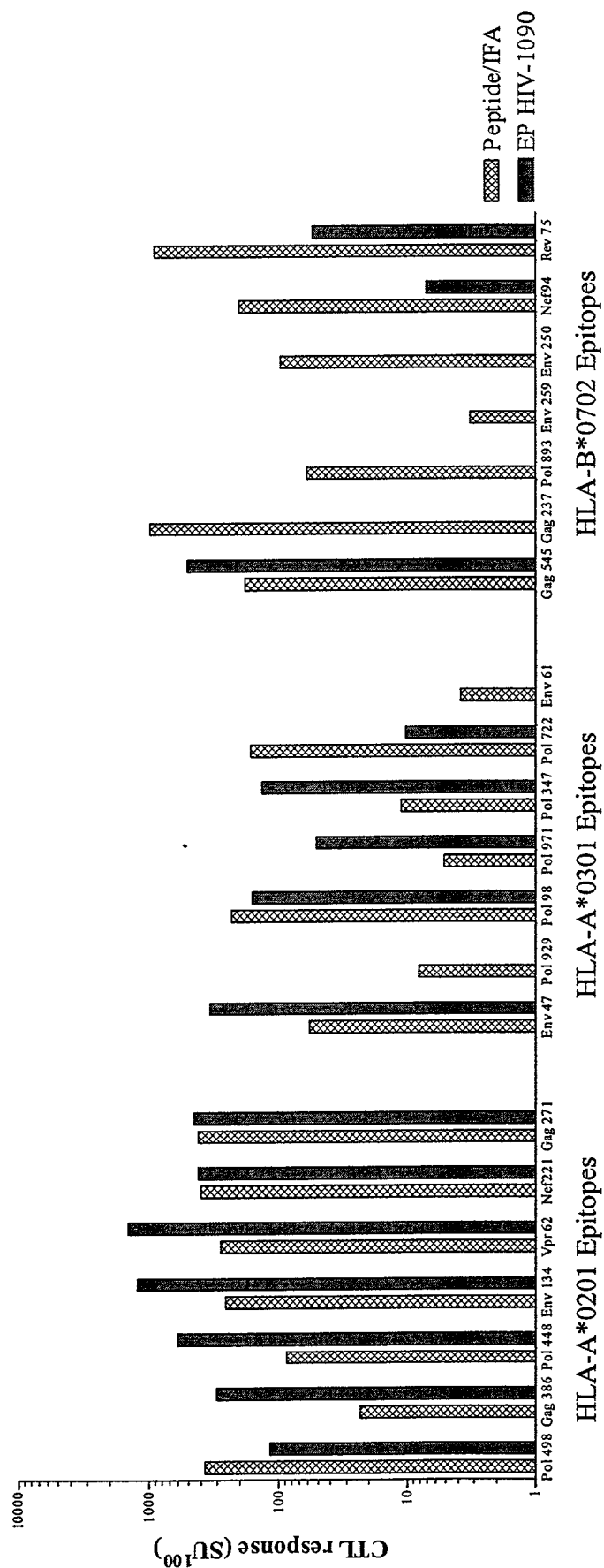


FIGURE 14A

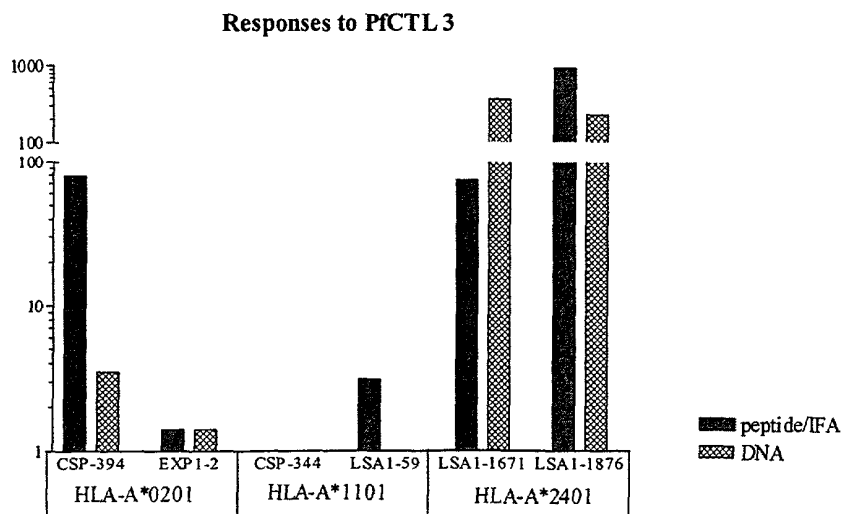
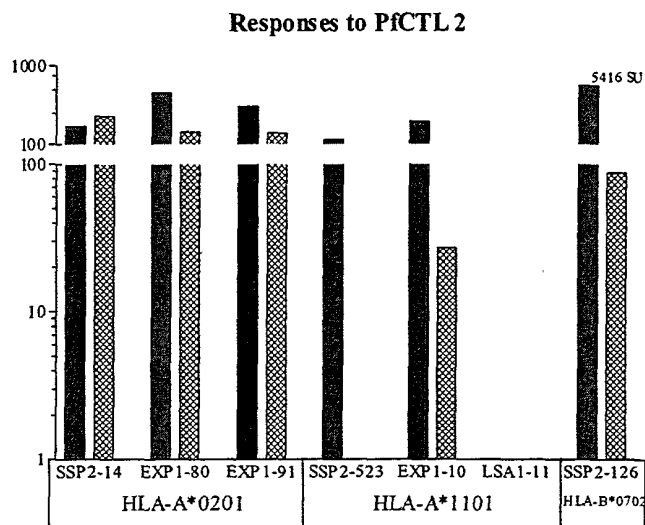
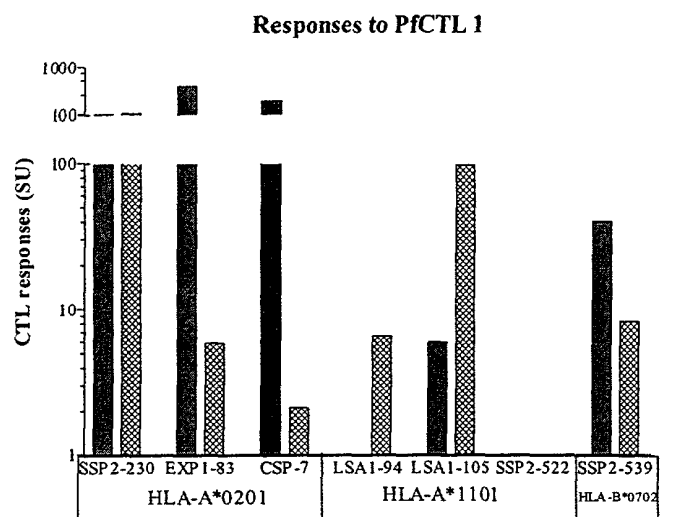
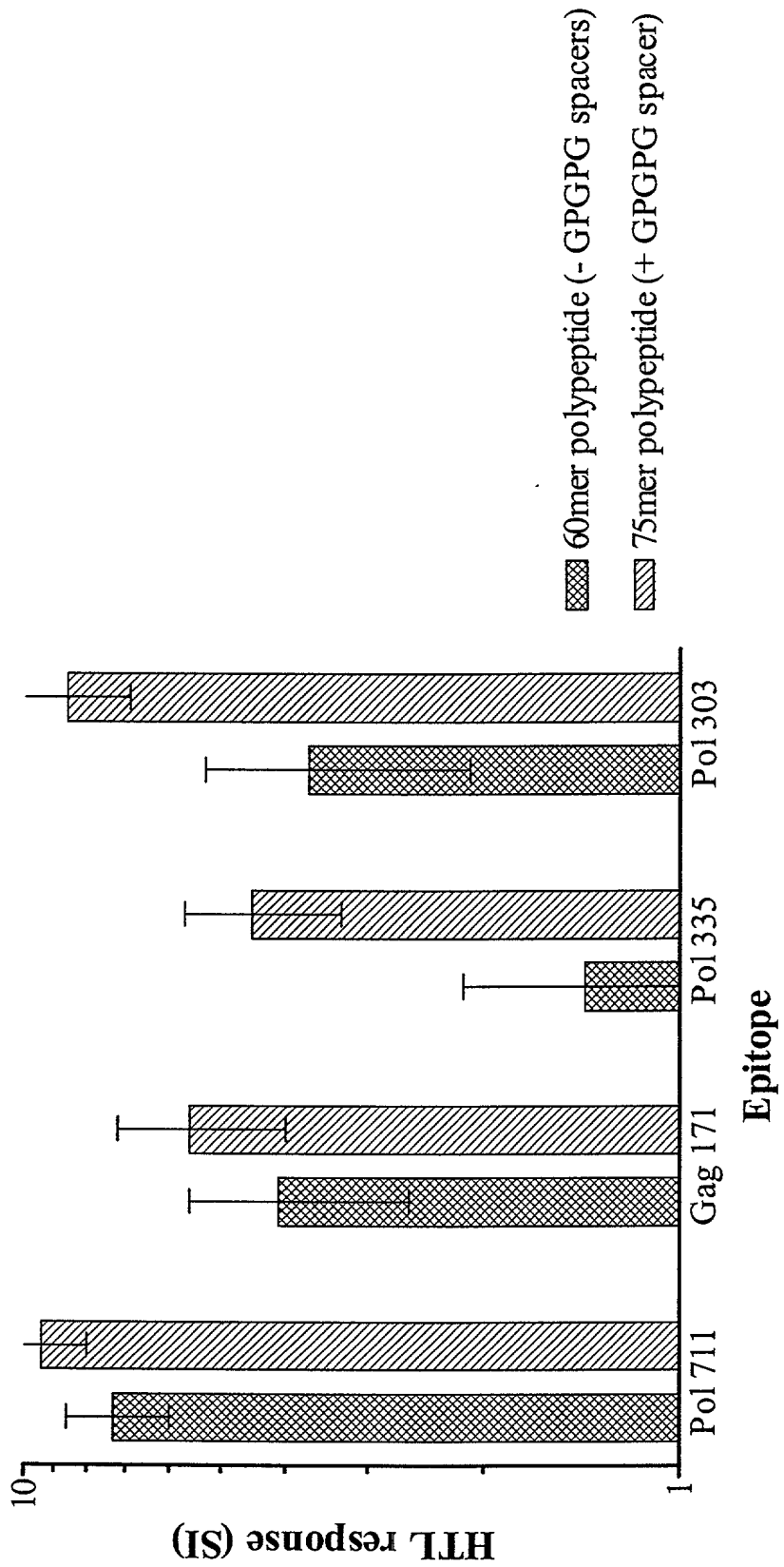


FIGURE 14B

FIGURE 15



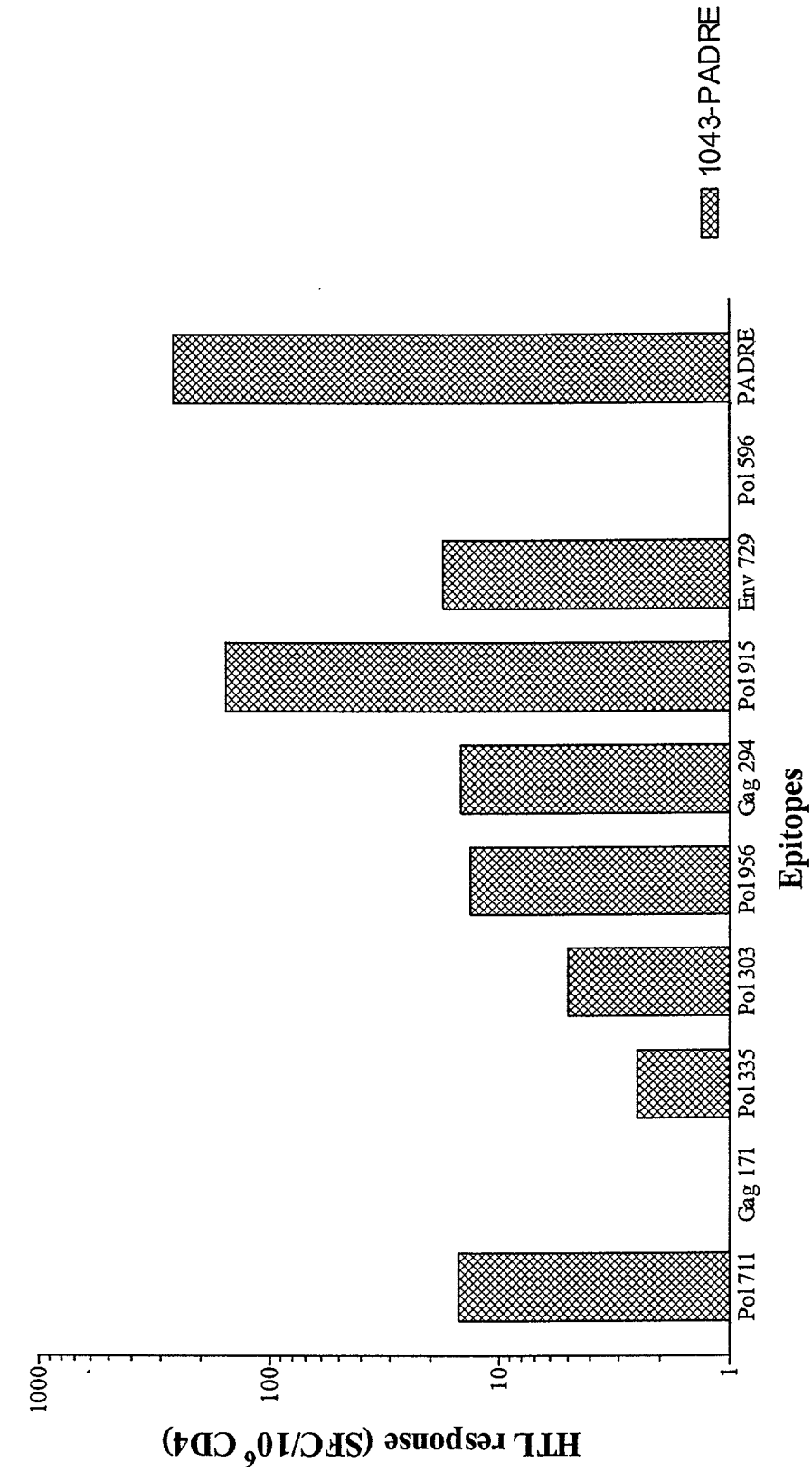


FIGURE 16

FIGURE 17

HIV 75mer

Pol 711	GPGPG	Gag 171	GPGPG	Pol 335	GPGPG	Pol 303
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EP HIV-1043

Pol 711/712	GPGPG	Pol 956	GPGPG	Pol 596	GPGPG	Vpu 31	GPGPG	Env 729	GPGPG	Gag 294/298	GPGPG	Gag 171	GPGPG	Env 566	GPGPG	Pol 874	GPGPG	Pol 915	GPGPG	Pol 335	GPGPG	Pol 674	GPGPG	Pol 758	GPGPG	Pol 619	GPGPG	Pol 989	GPGPG	Pol 303
-------------	-------	---------	-------	---------	-------	--------	-------	---------	-------	-------------	-------	---------	-------	---------	-------	---------	-------	---------	-------	---------	-------	---------	-------	---------	-------	---------	-------	---------	-------	---------

EP HIV-1043

Pol 711/712	GPGPG	Pol 956	GPGPG	Pol 596	GPGPG	Vpu 31	GPGPG	Env 729	GPGPG	Gag 294/298	GPGPG	Gag 171	GPGPG	Env 566	GPGPG	Pol 874	GPGPG	Pol 915	GPGPG	Pol 335	GPGPG	Pol 674	GPGPG	Pol 758	GPGPG	Pol 619	GPGPG	Pol 989	GPGPG	Pol 303	GPGPG	PADRE
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EP-HIV-1090

MGMQVQIQSLFLLLLWVPGSRGKLVGKLNWAGAAILKEPVHGVNAACPKVSFEPIKIPHYCAPA-  
KAKFVAAWTLKAAAKAFPVRPQVPLGAAKLTPLCVTLGAAAVLAEAMSQVKVYLAWVPAHKG  
AAAAIFQSSMTKKTTLFCASDAKNIPYNPQSQGVVKHPVHAGPIANVTVYYGVPVWKKAAAQMA  
VFIHNFKNAAAYPLASLRSLFNLTFGWCFKLNRLQQLLFINAKIQNFRVYYRKA AVTIKIGGQLKK  
VPLQLPPLKAMTNNPIPV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA  
GGAAAGCTGGTGGGCAAACCTCAACTGGGCCGGAGCTGCAATCCTGAAGGAGCCCGTCCACGG  
GGTGAATGCCGCTTGCCCTAAAGTCAGCTTCGAACCAATTAAGATCCCCATTACTACTGTGC  
ACCTGCCAAAGCTAAGTTTGTGGCCGCTTGACCCCTCAAGGCCGCTGCAAAAGCCTTCCCAGT  
GAGGCCCCAGGTGCCTCTGGGCGCCGCTAAACTCACACCACTGTGCGTCACTCTGGGAGCCGC  
TGCAGTGTCTGGCAGAGGCCATGTCCCAAGTGAAGGTGTATCTGGCTTGGGTGCCCCGCCACAA  
GGGGGCCGCTGCAGCCATCTTTCAGTCTAGCATGACCAAGAAAACAACTCTGTTCTGTGCCTC  
CGACGCTAAGAACATCCCTTATAATCCACAGTCTCAGGGCGTGGTCAAGCATCCCGTGCACGC  
CGGACCTATTGCTAACGTGACCGTGTACTATGGGGTCCCAGTGTGGAAGAAAGCCGCTGCACA  
GATGGCCGTGTTTATTCACAATTTCAAAAACGCCGCTGCATACCCCTCGCCAGCCTGAGATC  
CCTCTTCAACCTGACATTCGGCTGGTGTCTTAAAGCTGAACCGGATCCTGCAGCAACTGCTCTTT  
ATCAATGCTAAATCCAGAACTTCCGCGTCTACTATAGGAAGGCTGCAGTGACTATCAAAATT  
GGCGGACAACTGAAGAAAGTGCTCTCCAGCTGCCCCCTCTCAAGGCAATGACCAACAATCC  
CCCTATCCCAGTCTGA

HIV-CPT

MGMQVQIQSLFLLLLWVPGSRGIPIHYCAPAKAAKIQNFRVYYRKA AVTIKIGGQLKKAKFVAAW  
TLKAAAKVPLQLPPLKAIFQSSMTKKTPLCVTLGAQMAVFIHNFKGAKVYLAWVPAHKNAPYN  
PQSQGVVKAILKEPVHGVGAAALTFGWCFKLNAVLAEMSQVNRILQQLLFINAAACPKVSFEPI  
KVTVYYGVPVWKKAAHPVHAGPIANAAAYPLASLRSLFNAAATTLFCASDAKNKLVGKLNWAN  
AAAFPVRPQVPLNMTNNPIPV

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA  
GGAATCCCCATTCACTACTGCGCCCCTGCTAAGGCAGCCAAAATCCAGAACTTCAGGGTGTAT  
TACAGAAAGGCTGCAGTCACCATTAAAATCGGCGGACAACTGAAGAAAGCCAAGTTTGTGGC  
CGCTTGGACACTCAAGGCCGCTGCAAAGGTCCCACTGCAGCTCCCCCTCTGAAGGCCATCTT  
CCAGAGCTCCATGACTAAGAAACTGACCCCACTGTGTGTGACACTCGGGGCCAGATGGCTGT  
GTTTCATCCATAATTTTAAAGGCGCCAAGGTCTACCTGGCTTGGGTGCCCCGCACACAAGAACGC  
CATTCTTACAATCCACAGTCTCAAGGAGTGGTCAAAGCTATTCTGAAGGAGCCCGTGCACGG  
GGTGGGCGCCGCTGCACTCACTTTCGGATGGTGTCTTAAACTGAACGCCGTGCTGGCTGAAGC  
CATGAGCCAGGTCAATCGGATCCTGCAGCAACTGCTCTTCAATTAACGCCGCTGCATGTCCTAA  
GGTGTCTTCGAGCCAATCAAAGTGACCGTGTATTACGGGGTCCCCGTGTGGAAGAAAGCCGC  
TCATCCTGTCCACGCAGGCCCAATCGCCAACGCCGCTGCATATCCCTCGCCTCTCTGCGCAG  
CCTGTTTAAACGCCGCTGCAACAACCTCTTTTGCGCCTCCGACGCTAAGAATAAACTGGTGGG  
AAAGCTGAACTGGGCCAACGCAGCTGCATTCCTGTGAGGCCACAGGTCCCCCTCAATATGAC  
TAACAATCCCCCTATCCAGTGTGA

FIGURE 18A

HIV-FT

MQVQIQSLFLLLLWVPGSRGKLVGKLNWAMASDFNLPPVAIFQSSMTKVTIKIGGQLKRILQQLLF  
IMAVFIHNFKIPYNPQSQGVVTTLCASDAKILKEPVHGVQMAVFIHNFKGAAVFIHNFKRCPKVSF  
EPIKIQNFRVYYRLTFGWCFKLQVPLRPMTYKMTNPPPIVTVYYGVPVWKVLAEAMSQVPIHY  
CAPAKLTPLCVTL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAAG  
CTGGTGGGGAAGCTGAACTGGGCCATGGCCAGCGATTTCAACCTGCCCCCGTGGCCATCTTC  
CAGAGCAGCATGACCAAGGTGACCATCAAGATCGGGGGGCAGCTGAAGAGGATCCTGCAGCA  
GCTGCTGTTTCATCATGGCCGTGTTTCATCCACAACCTTCAAGATCCCCTACAACCCCGAGAGCCA  
GGGGGTGGTGACCACCCTGTTCTGCGCCAGCGATGCCAAGATCCTGAAGGAGCCCGTGCACG  
GGGTGCAGATGGCCGTGTTTCATCCACAACCTTCAAGGGCGCCGCCGTGTTTCATCCACAACCTTCA  
AGAGGTGCCCCAAGGTGAGCTTCGAGCCCATCAAGATCCAGAACTTCAGGGTGTACTACAGG  
CTGACCTTCGGGTGGTGCTTCAAGCTGCAGGTGCCCCTGAGGCCCATGACCTACAAGATGACC  
AACAACCCCCCATCCCCGTGACCGTGACTACGGGGTGCCCGTGTGGAAGGTGCTGGCCGAG  
GCCATGAGCCAGGTGATCCCCATCCACTACTGCGCCCCCGCCAAGCTGACCCCCCTGTGCGTG  
ACCCTG

0584038.062701  
T07290.8106860

**FIGURE 18B**



# HIV-TC

MGMQVQIQSLFLLLLWVPGSRGYWQATWIPEWKAIFQSSMTKKVYLAWVPAHKNAACP KVSFE-  
PIKHPVHAGPIANLTFGWCFKLNKMIGGIGGFIKFRDYVD RFYKAAARILQQLLFINTTLFCASDAK  
NQMVHQAISPRGAKLVGKLNWAGAAAIYETYGDTWKAAQVPLRPMTYKGAAAVTVLDVGDAY  
NAAARYLKDQQLNLNFPISPINMTNNPPIPVNAPYNTPVFAIKAAAVPLQLPPLKAAIPYNPQSQ  
GVVKALLQLTVWVGIGAILKEPVHGVNAAAFPISPIETVKVWKEATTTLFKAAAVTIKIGGQLK KI  
YQEPFKNLKAAAVLAEAMSQVNLVGPTPNIGAAAEVNIVTDSQYKAAAPIHYCAPAKAVIYQY  
MDDL YKAAAQMAVFIHNFKNAAATYQIYQEPFKPYNEWTL ELKAKIQNFRVYYRKA FVRPQVPL  
GAAAIWGC SGKLIKVMIVWQVDRNAAKAACWWAGIKAKFVAAWTLKAAAKLTPLCVTLNAAM  
ASDFNLPPVKSLLNATDIAVNVTVYYGVPVWKAAAAIIRILQQLKRAMASDFNLNAAAYPLASL  
RSLF

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGATCTAGA  
GGATACTGGCAAGCTACTTGGATTCCAGAATGGAAGCTATCTTTCAATCCTCAATGACGAAG  
AAGGTATACCTGGCATGGGTCCCAGCACACAAGAACGCCGCTTGCCCAAAGGTGTCCTTTGAA  
CCCATTAACACCCAGTGCACGCAGGGCCAATAGCGAATTTGACATTCGGGTGGTGCTTCAAA  
CTAAACAAAATGATCGGCGGCATTGGAGGCTTTATCAAGTTTAGAGATTACGTGGACCGATT  
TATAAAGCCGCTGCCCCGCTACTCCAGCAGCTACTATTCAACACCACTCTCTTCTGCGCTT  
CAGACGCTAAGAACCAAATGGTACACCAAGCCATAAGCCCTAGAGGAGCCAAGCTCGTAGGG  
AAATTAAATTGGGCGGGTGCAGCAGCAATCTACGAGACTTACGGCGATACCTGGAAGCAGC  
CCAGGTTCCGTTACGCCCAATGACCTATAAAGGCGCAGCAGCAGTAACAGTTCTAGATGTAGG  
AGACGCTTACAACGCTGCCGCAAGATACCTAAAAGATCAGCAGTTACTCAACACACTAAATTT  
CCCAATTAGCCCGATAAACATGACAAATAACCCACCAATTCCTCGTCAATGCTCCCTACAACAC  
TCCAGTATTCGCAATCAAAGCCGCTGCTGTCCCCCTGCAGCTCCCTCCTCTGAAAGCTGCGAT  
ACCTTACAACCCACAGAGCCAAGGTGTTGTCAAAGCACTGCTTCAGCTAACAGTTTGGGGAAT  
TGGTGCTGCAATTCTAAAAGAGCCAGTTCATGGGGTTAACGCCGCCGCTTCCCAATCAGTCC  
TATTGAGACTGTGAAAGTATGGAAAGAAGCCACAACCACACTTTTAAAGGCAGCCGCAGTTA  
CAATTAATAATAGGGGGCCAACTTAAGAAAATATACCAGGAACCTTTCAAGAATCTCAAAGCC  
GCTGCAGTGCTCGCCGAGGCTATGTCACAGGTGAATTTGGTCGGACCAACACCCGTAAACATC  
GGAGCCGCAGCCGAAGTGAACATAGTCACCGACTCACAGTACAAAGCCGCTGCAATACCCAT  
ACATTATTGTGCTCCCGCAAAGGCCGTGATCTATCAATATATGGACGACCTGTATAAGGCCGC  
CGCGCAGATGGCAGTCTTTATCCACAACCTTTAAAAACGCAGCTACTTATCAGATCTACCAGGA  
ACCATTCAAACCGTACAATGAGTGGACCTTGGAATAAGGCCAAAATTCAGAACTTCAGGG  
TATATTATAGAAAAGCATTTCCAGTGAGGCCCCAGGTGCCTCTGGGTGCCGAGCAATATGGG  
GATGTTCTGGAATACTGATCAAGGTGATGATTGTATGGCAAGTGGACAGAAATGCAGCTAAG  
GCAGCCTGTTGGTGGGCAGGTATAAAGCAAAGTTCGTGGCAGCATGGACGCTTAAAGCAGC  
CGCAAAACTCACTCCTCTCTGCGTGACACTTAATGCAGCCATGGCCTCTGATTTCAACCTTCCC  
CCTGTAAAATCCCTGCTTAATGCGACAGATATCGCAGTCAACGTAACAGTATATTATGGCGTG  
CCAGTCTGGAATAAGCCGCCGCGGCCATAATTCGGATACTGCAGCAGCTGAAAAGAGCTAT  
GGCGAGTGACTTCAACCTGAATGCGGCCGCTACCCCTTGGCATCGTTAAGGTCACTATTTTG

A

FIGURE 18C

HCV.1

MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVDLMGYIPLVYL VAYQATVILAGY GAGVRLIVFP  
DLGVHMFNFISGIYLLPRRGPRLYLVTRHADVVLVGGVLAALLFLLLADAFLLLADARVWMNRL  
IAFACTCGSSDLYLSAFSLHSYGVAGALVAFKLPGCSFSIFKTSERSQPRLIFCHSKKKFWAKHMW  
NFIPFYGKAIRMYVGGVEHRQLFTFSPRRRLGVRATRKVGIYLLPNRAKFVAAWTLKAAA\*

GAATTCGCCGCCACCATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGACTGC  
TGTTCAACATCCTGGGGGGGTGGGTGGATCTGATGGGGTACATCCCCCTGGTGTACCTGGTGGCCTACCAGGCCACCGT  
GATCCTGGCCGGGTACGGGGCCGGGGTGAAGCTGATCGTGTCCCCGATCTGGGGGTGCACATGTGGAACCTTCATCAGC  
GGGATCTACCTGCTGCCAGGAGAGGACCTAGACTGTACCTGGTGAAGTACACGCTGATGTGGTGTGGTGGGAGGAG  
TGCTGGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTTTCCTGCTGCTGGCTGATGCTAGAGTGTGGATGAACAGACT  
GATCGCTTTCGCTTGTACATGTGGAAGCTCCGATCTGTATCTGAGCGCTTTCAGCCTGCACAGCTACGGAGTGGCTGGA  
GCTCTGGTGGCTTTTAAGCTGCCTGGATGTAGCTTTAGCATCTTTAAGACCAGCGAAAGAAGCCAGCCTAGACTGATCT  
TTGTGCACAGCAAGAAGAAGTTTGGGCTAAGCACATGTGGAATTTTATCCCTTTCTATGGAAAGGCTATCAGAATGTA  
TGTGGGAGGAGTGGAAACAGACAGCTGTTTACATTTAGCCCTAGAAGGAGACTGGGAGTGAGAGCTACAAGAAAGGTG  
GGAATCTATCTGCTGCCTAATAGATGAAAGCTTGGG\*

HCV.2

MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAALLFLLLADALIFCHSKKKQLF  
TFSPRRYLVTTRHADVYLLPRRGPRLCTCGSSDLYHMFNFISGIFWAKHMWNFAKFVAAWTLKAA  
AILAGY GAGVYL VAYQATVGVAGALVAFKIPFYGKAIRMYVGGVEHRVLVGGVLAALLFLLLADA  
RVLPGCSFSIFAKFVAAWTLKAAAKTSERSQPRRLGVRATRKRLIVFPDLGVWMNRLIAFALSFS  
LHSYLLFNILGGWVVGIIYLLPNR\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCGGATCCAGAGGAGATCTGATGGGATATATCCCTCTGGTGGCTAAGTTTGTGGCTGCT  
TGGACACTGAAGGCTGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTCTGATCTTCTGTCA  
GCAAGAAGAAGCAGCTGTTTACATTTAGCCCAAGAAGATATCTGGTGACAAGACACGCTGAT  
GTGTATCTGCTGCCTAGACGCGGACCTAGACTGTGTACATGTGGAAGCTCCGATCTGTATCAC  
ATGTGGAACCTTTATCAGCGGAATCTTTTGGGCTAAGCACATGTGGAATTTTCATCCTGGCTGGA  
TATGGAGCTGGAGTGTATCTGGTGGCTTATCAGGCTACAGTGGGAGTGGCTGGAGCTCTGGTG  
GCTTTCAAGATCCCATTTCTATGGAAAGGCTATCAGAATGTATGTGGGAGGAGTGGAAACACAG  
AGTGTCTGGTGGGAGGAGTGTCTGGCTGCTTTCCTGCTGCTGGCTGATGCTAGAGTGTCTGCCAGG  
ATGTAGCTTTAGCATCTTCAAGACTTCCGAACGCTCCCAGCCTAGAAGACTGGGAGTGAGAGC  
TACAAGGAAGAGACTGATCGTGTTCAGATCTGGGAGTGTGGATGAATAGACTGATCGCTTT  
CGCTCTGAGCGCTTTTACGCTGCACAGCTATCTGCTGTTCAACATCCTGGGAGGATGGGTGGT  
GGGAATCTATCTGCTGCCAAACAGATGAAAGCTT

HCV.3s1

MGMQVQIQSLFLLLLWVPGSRGYLVAYQATVAKFVAAWTLKAAALLFLLLADALIFCHSKKKYL  
VTRHADVLGFGAYMSKCTCGSSDLYHMFNFISGIFWAKHMWNF\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCGGATCCAGAGGATACCTCGTCGCTACCAGGCCACTGTGGCTAAATTCGTGGCAGCC  
TGGACACTGAAAGCTGCAGCTCTGCTCTTCTGCTCCTGGCCGATGCACTCATCTTCTGCCATT  
CCAAGAAAAAGTATCTGGTCACCAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAGC  
AAGTGACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACCTTTATTTCTGGAATCTTTTGGG  
CCAAGCACATGTGGAATTTCTGAAAGCTT

FIGURE 18D

HCV.3s2

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLLADARVLSAFSLHSYIL -  
AGYGAGVWMNRLIAFAIPFYGKAIVAGALVAFKVGIYLLPNR\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGATCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTGCTGCT  
TGGACACTGAAGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGC  
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT  
GCCATTCCATTCTATGGGAAAGCCATTGTGGCTGGCGCCCTGGTGGCATTCAAGGTCGGGATC  
TACCTCCTGCCTAACCGCTGAAAGCTT

HCV.3s2(-3)

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLLADARVLSAFSLHSYIL  
AGYGAGVWMNRLIAFA\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGATCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTGCTGCT  
TGGACACTGAAGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGC  
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT  
GCCTGAGGATCC

HCV.3s3

MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAARLGVRATRKLNFILGGWV  
RMYVGGVEHRRLLIVFPDLGVGVAGALVAFKLPGCSFSIFKTSERSQPRQLFTFSPRRYLLPRRGPRL

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGATCCAGAGGAGACCTGATGGGCTACATCCCTCTCGTGGCCAAGTTTGTGGCAGCT  
TGGACCCTGAAGGCCGCTGCCAGACTGGGAGTGC GCGCTACACGGAAACTCCTGTTTAACATC  
CTGGGAGGGTGGGTGCGGATGTACGTCGGAGGCGTCGAGCACAGAAGGCTCATTGTCTTTCC  
AGATCTCGGCGTGGGCGTCGCAGGCGCACTCGTGGCCTTCAAAGTCCAGGGTGCAGCTTCAG  
CATTTTCAAGACCTCCGAACGCTCCCAACCCAGACAGCTGTTCACTTTCTCTCCTCGGAGGTAT  
CTGCTGCCAGACGCGGACCCAGGCTGTGAAAGCTT

HCV.PC3

MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVKAKFVAAWTLKAAALADGGCSGGAYRLIVFPD  
LGVKFWAKHWMNFIGVAGALVAFKKQLFTFSPRR\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGATCCAGAGGACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCCAAGTTCGTG  
GCTGCCTGGACCCTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCGGAGCTTACAG  
GCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGAATTTTCATCGG  
GGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCAAGACGGTGAGG  
TACC

FIGURE 18E

HCV.PC4

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAKFVAAWTLKAAAKTSERSQPRNLPGCSFSIFN  
DLMGYIPLVKYLLPRRGPRNLNLCGFADLMGYRMYVGGVEHR\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGATCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCCAAGTTCGTGGC  
TGCCTGGACCCTGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTG  
GATGCTCTTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCC  
CAGACGGGGCCCTCGCCTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTA  
TGTCGGCGGAGTCGAACACAGATGAGGTACC

HCV.2431(1P)

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAFLLADARVLSAFSLHSYILAGYGAGVWMNRL  
IAFAGAAARLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVKYLLPRRGPRNLNLCG  
FADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFPDLGVKFWAKHMWN  
FIGVAGALVAFKKQLFTFSPPRNGYLVAYQATVAAALLFLLADALIFCHSKKKYLVRHADVLG  
FGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKAAAAKFVAAWTLKAAA

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGCTCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGCTCCTGGCA  
GACGCCAGGGTGCTGTCTGCCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGC  
GTGTGGATGAATCGGCTGATCGCCTTTGCCGGCGCTGCCGCAAGGCTGGGCGTGAGAGCCACC  
CGGAAGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTC  
TTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGG  
GGCCCTCGCCTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGC  
GGAGTCGAACACAGAAAACCTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCT  
GGCCGACGGGGGATGCAGCGGGGAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAA  
ATTTTGGGCAAAGCACATGTGGAATTTATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAA  
GCAGCTCTTACCTTCTCCCCAAGACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGC  
TGCAGCTCTGCTCTTCTGCTCCTGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTAT  
CTGGTCACCAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGC  
AGCTCCGACCTGTATCACATGTGGAACCTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGG  
AATTTTAAGGCCGCAGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAGG  
ATCC

FIGURE 18F

# HCV.4312(1P)

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAATAKTSERSQPRNLPGCSFSIFNDLMGYIPLVK-YLLPRRGPRNLTLGCFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFPDLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRRNGYLVAYQATVAAALLFLLLADALIFCHSKKKYLVTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKKAAAVLVGGVLAAAFLLLADARVLSAFSLHSYILAGYGAGVWMNRLIAFANAAKFVAAWTLKAAA\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGCTCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAAAC AAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTCTTTCAGCATCTTTAATGACCTCAT GGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGGCCCTCGCCTGAACACTCTCTG TGGATTGCTGATCTGATGGGGTACAGGATGTATGTCGGCGGAGTCGAACACAGAAAAGTGTCTTCAACATCCTGCGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCG GAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGA ATTTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAA GACGGAACGGATACCTCGTCGCTACCAGGCCACTGTGGCTGCAGCTCTGCTCTTCCTGCTCC TGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACG TGCTGGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGT GGAACCTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGGAATTTTAAGAAAGCCGCTGCAG TCCTGGTGGGCGGCGTCTGGCAGCCGCTTTCTGCTCCTGGCAGACGCCAGGGTGTGTCTG CCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGA TCGCCTTTGCCAATGCTGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAG GATCC

## AOSL.K

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPDFFPSVKFLLSLGIH LYMDDVVLGVGLSRYVARLFLTRILTISTLPETTIVRRQAFTFSPTYKWLSLLVPFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG AAGGCTGCCGCTTTCTGCTAGCGATTTCTTTCTAGCGTGAAGTTCCTGCTGTCCCTGGGAA TCCACCTGTATATGGATGACGTGGTGTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT TCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG CCTTCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGGCCTTTGTGTGA

## HBV.1

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPDFFPSVFLSLGIHL YMDDVVLGVGLSRYVARLFLTRILTISTLPETTIVRRQAFTFSPTYKWLSLLVPFVPIIPSSWAFTP ARVTGGVFKVGNFTGLYLPDFFPSVTLWKAGILYKNVSIPWTHKLVDVFSQFSRSAICSVVRRAL MPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG AAGGCTGCCGCTTTCTGCTAGCGATTTCTTTCTAGCGTGTTCCTGCTGTCCCTGGGAATCC ACCTGTATATGGATGACGTGGTGTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCC TGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGGCCT TCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGGCCTTTGTGATCCCTATCCCTAG CTCCTGGGCTTTACCCCCAGCCAGGGTGACCGGAGGAGTGTTTAAGGTGGGAAACTTCACCGG CCTGTATCTGCCAGCGATTTCTTTCTAGCGTGACCCTGTGGAAGGCCGGGATCCTGTACAA GAATGTGTCCATCCCTTGGACCCACAAGCTGGTGGTGGACTTTTCCAGTTCAGCAGATCCGC TATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGTATGCCTGTATCTGA

FIGURE 18G

TC290-804650

HBV.2

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFPSDFFPSVNFLLSLGIH-  
LYMDDVVLGVGLSRYVARLFLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPI  
SSWAFKTPARVTGGVFKVGNFTGLYNLPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVD FSQ  
FSRNSAICSVVRRALMPYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGA  
GGACACACCCTGTGGAAGGCCGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG  
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGAACCTCCTGCTGTCCCTGGGAA  
TCCACCTGTATATGGATGACGTGGTGTCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT  
TCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG  
CCTTACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCTGCTGGTGCCCTTTGT  
GAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCAGCCAGGGTGACCGGAGGAGTGTT  
TAAGGTGGGAAACTTCACCGGCCTGTATAACCTGCCAGCGATTTCTTTCCTAGCGTGAAGAC  
CCTGTGGAAGGCCGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCG  
CTCTGGTGGTGGACTTTTCCAGTTCAGCAGAAATTCCGCTATCTGCTCCGTGGTGAGGAGAG  
CTCTGATGCCACTGTATGCCTGTATCTGA

PfCTL.1

MQVQIQSLFLLLLWVPGSRGILSVSSFLFVNAAAQTNFKSLLRNLPSENERGYKAAALLACAGLAY  
KKAAAKFVAAWTLKAAAKAFMKAVCEVNAAAFLFVEALFNATPYAGEPAPFKAAAKYKLA  
TSVLKAGVSENIFLNAAAAYFILVNLLIKAGLLGVVSTV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA  
GGAATCCTGAGCGTGTCTCTTTCCTGTTTGTCAACGCCGCTGCACAGACCAATTTCAAGAGC  
CTCCTGAGGAACCTCCCTCCGAGAACGAAAGAGGCTACAAAGCCGCTGCACTGCTCGCCTGC  
GCTGGACTGGCCTATAAGAAAGCCGCTGCAGCCAAGTTCGTGGCCGCTTGGACACTGAAGGC  
CGCTGCAAAAGCCTTTATGAAGGCTGTCTGTGTGGAGGTCAATGCCGCTGCATCTTTCCTGTTT  
GTGGAGGCCCTCTTTAACGCTACTCCTTACGCAGGGGAACCAGCCCCCTCAAGGCCGCTGCA  
AAATATAAGCTGGCAACCAGCGTGTCTGAAGGCTGGCGTGTCCGAGAATATTTTCTGAAAAAC  
GCCGCTGCATACTTCATCCTGGTGAATCTGCTCATTAAAGCCGGACTCCTGGGGGTGGTCTCT  
ACAGTGTGA

PfCTL.2

MQVQIQSLFLLLLWVPGSRGFVEALFQEYNAAAKYLIVVFLINALACAGLAYKKFYFILVNLLKA  
ALFFIIFNKNAAAKFVAAWTLKAAAKFILVNLLIFHNFQDEENIGIYKLPYGRNLKAAAVLLGGV  
GLVLNLIFFDLFLVKAVLAGLLGVV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA  
GGATTCGTGGAGGCCCTGTTTCAGGAATACAACGCCGCTGCAAAGTATCTCGTCATCGTGTTT  
CTGATCAATGCTCTGGCATGCGCCGGCCTCGCTTACAAAAAGTTTTACTTCATTCTGGTCAACC  
TGCTCAAGGCCGCTCTGTTCTTTATCATTTTCAATAAAAAACGCCGCAGCTAAGTTTGTGGCCGC  
ATGGACCCTGAAGGCCGCTGCAAAATTCATCCTCGTGAATCTGCTCATTTTTCAAACTTCCAA  
GACGAGGAAAATATCGGAATTTATAAGCTGCCCTACGGGAGGACAAACCTGAAAGCCGCTGC  
AGTCCTGCTCGGCGGAGTGGGGCTGGTGCTCAATTTTCTGATCTTCTTGATCTGTTCTCTGGT  
AAGGCCGCTCCTGGCCGGCCTGCTCGGAGTCGTGTGA

FIGURE 18H

PfCTL3

MQVQIQSLFLLLLWVPGSRGVFLIFFDLFLNAAAPSDGKCNLYKAAAVTCGNGIQVRKLFHIFDGD  
NEIKAHVLSHNSYEKNYYGKQENWYSLKKILSVFFLANAAAKFIKSLFHIFKAAALYISFYFIKAKF  
VAAWTLKAAAKAAAYYIPHQSSLKAAAGLMVLSFL

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA  
GGAGTGTTCTGATCTTCTTTGACCTGTTCTGAACGCCGCTGCACCCAGCGATGGCAAGTGC  
AATCTCTACAAGGCCGCTGCAGTGACCTGTGGAAACGGGATTCAGGTGAGGAACTCTTTCAC  
ATCTTCGACGGCGATAACGAGATCAAGGCCCATGTGCTGTCCACAATTCTTATGAAAAAAC  
TACTATGGAAAGCAAGAGAATTGGTACAGCCTGAAGAAAATTCTGTCCGTGTTCTTTCTCGCC  
AACGCCGCTGCAAAGTTTATCAAGTCTCTGTTCCATATTTTCAAGGCCGCTGCACTCTACATCA  
GCTTCTATTTTATTAAAGCCAAATTTGTGGCCGCTTGGACACTGAAGGCCGCTGCAAAAGCCG  
CTGCATACTATATCCCTCACCAGAGCTCCCTGAAGGCCGCTGCAGGGCTGATCATGGTGCTCT  
CTTTCCTGTGA

PfCTL/HTL(N)

MQVQIQSLFLLLLWVPGSRGSSVFNVNSSIGLMVLSFLGPGPGLYISFYFILVNLLIFHINGKIIKN  
SEGPGPDPDSIQDSLKESRKLSGPGPGLVLAGLLGVVSTVLLGGVGLVLGPGPGLPSENERGYYPH  
SSLGPGPGQTNFKSLRLNLGVSENIFLKGPFGFQDEENIGIYGPFGPKYLVIVFLIFFDLFLVGP  
GKFIKSLFHIFDGDNEIGPFGPKSKYKLATSVLAGLLGPGPGLPYGKTNLGPGRHNVNHA  
VPLAMKLIGPFGMRKLAILSVSSFLFVEALFQEYGPFGPVTCGNGIQVRGPFGMNYGKQENWYSL  
KKGPFGPSPDGKCNLYADSAWENVKNVIGPFMKAVCVEVGPFGPKILSVFFLALFFIIFNKGPFG  
HVLSHNSYEKGPGPKYKIAGGIAGGLALLACAGLAYKFVVPGAATPYAGEPAPF

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA  
GGAAGTAGTGTTCAATGTTGTGAACCTCATCAATTGGTCTGATCATGGTGCTGAGCTTTCTCG  
GGCCAGGGCCAGGATTATATATTTCTTTCTACTTCATCCTTGTCACCTGTTAATATTCCACAT  
TAACGGCAAAATAATAAGAACAGTGAAGGCCCTGGGCCTGGGCCTGACTCGATCCAGGATT  
CTCTAAAAGAAATCGAGGAAGCTCTCCGGACCAAGGCCCTGGTGTACTCGCCGGGTGCTGGGA  
GTAGTTAGCACAGTGCTGTTAGGAGGCGTCGGCCTCGTCTTAGGACCTGGACCAAGTCTGCCG  
TCCGAAAACGAAAGAGGATACTACATACCTCACCAGAGCAGCCTCGGCCCAGGCCCCGGACA  
AACCAATTTCAAATCCCTCTTGCGAAATCTAGGAGTGAGCGAGAACATATTTCTTAAAGGACC  
CGGTCCCGGCTTTCAGGACGAGGAGAAATATAGGTATTTACGGTCCAGGACCTGGAAAATACCT  
AGTGATCGTATTCTAATTTTTTTTGTGACCTATTTCTGGTGGGCCAGGTCCCGGAAAGTTCATT  
AAATCACTCTTCCACATTTTTTGTGACGAGATAACGAGATAGGACCCGGTCCCGGAAATCAA  
GTACAAACTAGCCACTTCAGTGCTGGCCGGCCTTCTAGGGCCGGGCCAGGGCTCCCCTATGG  
AAAGACAAATCTTGCCCCGGTCCAGGACGGCACAACCTGGGTGAATCATGCGGTTCCATTGG  
CCATGAAACTAATCGGGCCCGGTCCAGGCATGCGCAAACTTGAATTCTAAGCGTAAGTTCAT  
TTCTGTTTCGTAGAGGCACTGTTTCAAGAATATGGCCCAGGACCTGGCGTCACATGTGGGAATG  
GGATCCAGGTGAGAGGACCGGGACCTGGTATGAACCTATTACGGTAAACAGGAAAATTGGTAC  
TCCCTGAAAAAGGGTCCAGGCCCCGGCCCCCTCAGATGGTAAGTGCAACCTGTATGCTGACTCA  
GCATGGGAGAACGTAAAAAATGTAATAGGCCCATTCATGAAGGCAGTTTGTGTGCAAGTCCG  
ACCAGGCCAGGAAAAATACTTTCTGTCTTCTTCTAGCTCTCTTCTTCATCATCTTCAACAAG  
GGACCAGGGCCAGGTACGTGTTATCCATAACTCTTATGAAAAAGGGCCAGGACCTGGGAA  
ATACAAAATCGCAGGAGGGATCGCCGGCGGGCTAGCGCTCCTTGCTGCGCAGGCTTGCTTA  
CAAATTCGTTGTACCAGGAGCTGCAACACCCTATGCAGGAGAACCTGCCCCATTTTGAAGATC  
TGC

FIGURE 18I

Pf33

MGMQVQIQSLFLLLLWVPGSRGFMKAVCDEVNVTGNGIQVRKGLIMVLSFLNAALFHIFDGDN \_  
EIKAAALLACAGLAYKKSFLFVEALFNAAPSDGKCNLYKAAQTNFKSLLRNLPSENERGYKAAGVS  
ENIFLKNAAYFILVNLLIKAAAILSVSSFLFVNTPYAGEPAPFKAAAKYKLATSVLKAAVFLIFFDL  
FLNYYIPHQSSLKAAGLLGNVSTVGAVLLGGVGLVNLACAGLAYKKAKFIKSLFHIFKAAFYFIL  
VNLLKAFLIFFDLFLVKALFFIIFKNYYGKQENWYSLKFVEALFQEYNAAAKFVAAWTLKAAAK  
ILSVFFLANAVLAGLLGNVNFQDEENIGIYKAAALYISFYFIKAFILVNLLIFHNAALPYGRTNLKAA  
HVLSHNSYEKNAAAKYLVIVFLI

GCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCC  
GGATCCAGAGGATTTATGAAAGCTGTCTGTGTAGAGGTGAATGTAACATGCGGTAACGGAAT  
TCAGGTGAGAAAGGGACTCATCATGGTACTCAGCTTTCTGAACGCAGCCCTGTTCCACATCTT  
TGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCCTGTGCCGGACTAGCCTATAAAAAGA  
GTTTCTTTTTCGTTGAAGCACTATTTAACGCAGCACCCAGTGACGGTAAATGCAACCTATATA  
AAGCAGCTCAGACTAATTTCAAAGCCTGTTAAGAAATCTGCCCTCAGAGAATGAAAGGGGT  
TACAAAGCCGCCGGCGTGTCCGAGAATATTTTCTGAAGAACGCCGCTGCTTATTTTATACTC  
GTGAATCTACTCATAAAGGCAGCCGCAATCCTTTTCAGTGTCCAGCTTTCTGTTTGTAAACACAC  
CATATGCGGGCGAGCCGCTCCTTTCAAGGCTGCAGCAAAATACAAGCTTGCCACATCAGTAT  
TGAAAGCAGCTGTGTTTTGATATTCTTTGATCTTTTTTAACTACTACATACCTCATCAGTCT  
AGTCTTAAAGCAGCCGGGCTACTGGGGAACGTCTCTACTGTGGGGGCGCTTACTTGGAGGA  
GTTGGCCTCGTGTGAACCTCGCGTGCGCAGGTCTGGCCTACAAAAAGCGAAATTCATCAAG  
TCTCTGTTCCACATTTTTAAAGCCGCATTCTATTTCACTAGTGAACCTTCTCAAAGCTTTCT  
GATCTTCTTCGATCTATTCCTCGTAAAAGCGCTATTCTTCATTATCTTTAAACAAAAATTATTAC  
GGCAAGCAAGAAAAATTGGTACTCAAGTTTGTAGAAGCTCTGTTCCAGGAATACAACGCC  
GCTGCTAAATTCGTTGCAGCTTGGACCCTGAAAGCAGCTGCAAAGATCCTATCGGTCTTCTTTC  
TCGCTAATGCCGTATTAGCAGGACTTCTAGGCAACGTGAACCTTCAAGACGAAGAGAATATAG  
GCATCTACAAAGCCGCAGCACTGTACATTTCTACTTCAAGGCCTTCATACTGGTCAA  
CCTTCTGATATTTATAATGCAGCACTGCCATATGGGAGAACCAACTTGAAAGCGGCCACGT  
GTTGAGCCACAACCTCTACGAGAAGAACGCCGCCGCGAAATATCTCGTCATTGTCTTCTCTGAT  
TTGA

TB.1

MQVQIQSLFLLLLWVPGSRGRMSRVTTFTVKALVLLMLPVVNLMIQTAAAVVKALVLLMLPVGA  
GLMTAVYLVGAAAMALLRLPVKRMFAANLGVNSLYFGGICVGRPLPLPAVNAAAACFVAAWT  
LKAAAKAAARLMIGTAAAGFVVALIPLVNAMTYAAPLFVGAAAAMALLRLPLV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGATCCAGAGGAAGG  
ATGAGCAGAGTGACCACATTCAGTGTCAAGGCCCTGGTGTCTCTGATGCTCCCCGTCGTGAAC  
CTGATGATCGGCACCGCTGCAGCCGTCGTGAAAGCTCTCGTCCTGCTCATGCTCCCTGTGGGA  
GCAGGGCTGATGACAGCCGTGTACCTGGTCCGGCGCTGCAGCCATGGCCCTCCTGCGGCTGCCA  
GTGAAGCGCATGTTTGCTGCAAATCTGGGAGTCAACTCCCTCTATTTTCGGGGGCATTGCGGTG  
GGAAGGCTGCCCTCGTGTGCTGCTGTGAATGCAGCCGCTGCCAAATTTGTCGCCGCTTGG  
ACTCTGAAGGCAGCCGCTAAGGCCGCTGCAAGACTGATGATCGGGACCGCCGCTGCCGGCTT  
CGTGGTCCGCCCTGATTCCTTGGTGAACGCCATGACATACGCAGCTCCTCTGTTTGTGGGAGC  
CGCTGCAGCCATGGCTCTCCTGCGGCTGCCACTGGTGTGA

FIGURE 18J



BCL A2 #90

MQVQIQSLFLLLLWVPGSRGIMIGHLVGVNRLQETELVNAKVAEIVHFLNAKVFGSLAFVNAYL-  
SGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGTRVNAAA  
ATVGIMIGVNAKLCPVQLWV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGAGGAATT  
ATGATCGGCCATCTGGTGGGCGTCAACAGACTGCTGCAGGAAACCGAGCTGGTGAATGCCAA  
GGTGGCCGAAATTGTGCACTTTCTCAACGCAAAGGTGTTTGGTTCCTGGCTTTTGTCAATGCC  
TATCTGAGCGGCGCTAACCTCAACGTCGGAGCCGCTACCTCCAGCTGGTCTTCGGCATCGAG  
GTCAACGCTGCTGCAAAATTCGTGGCAGCTTGGACCCTCAAGGCTGCAGCAAAGGCTGCCGCC  
GTCGTGCTCGGAGTGGTGTTCGGGATCAACTCTATGCCACCTCCCGGGACTAGGGTCAATGCT  
GCCGCCGCAACAGTGGGAATCATGATTGGGGTGAATGCCAACTGTGCCCAGTGCAACTGTG  
GGTGTGA

BCL A2 #88

MQVQIQSLFLLLLWVPGSRGVVLGVVFGINAAAKFVAAWTLKAAAKVAEIVHFLNAYLSGANL  
NVGAAYLQLVFGIEVNIMIGHLVGVNRLQETELVNAKVFGSLAFVNAKLCPVQLWVNAAAATV  
GIMIGVNSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGAGGAGTC  
GTGCTGGGAGTCGTCTTCGGCATTAATGCCGCCGCTGCAAAGTTCGTGGCTGCCTGGACCCTG  
AAGGCCGCAGCTAAAGTGGCAGAGATCGTGCACTTTCTGAACGCCTACCTGAGCGGAGCAAA  
TCTGAACGTCGGCGCTGCCTATCTGCAGCTCGTGTTTGAATTGAAGTGAACATCATGATTGG  
ACATCTGGTGGGCGTGAACAGGCTGCTCCAGGAACTGAGCTGGTCAACGCTAAAGTGTTCG  
GGTCTCTCGCCTTTGTGAACGCTAAGCTCTGCCCCGTCCAACTCTGGGTCAATGCCGCAGCCG  
CTACAGTGGGGATCATGATCGGCGTGAACCTCATGCCTCCACCAGGGACCAGAGTGTGA

BCL A2 #63

MQVQIQSLFLLLLWVPGSRGKLCVPVQLWVNAAAATVGIMIGVNIMIGHLVGVNRLQETELVNA  
KVAEIVHFLNAKVFGSLAFVNAYLSGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAA  
AVVLGVVFGINSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGAGGAAAG  
CTCTGCCCCGTGCAACTGTGGGTCAACGCCGCCGCCGCAACCGTCGGCATTATGATCGGGGTG  
AACATCATGATCGGACACCTGGTCGGCGTGAACAGGCTGCTGCAGGAGACAGAACTGGTCAA  
TGCCAAGGTGGCTGAAATTGTCCATTTCTGAATGCCAAAGTGTTTCGGCTCTCTCGCTTTCTG  
AACGCTTATCTGAGCGGAGCTAACCTCAACGTGGGGGCCGCATACCTCCAGCTCGTCTTTGGG  
ATTGAGGTGAATGCCGCAGCTAAATTTGTGCTGCCTGGACCCTGAAGGCAGCAGCCAAGGCT  
GCCGCAGTGGTGTGGGAGTGGTGTGGAATCAATTCCATGCCTCCACCAGGCACTAGAGTG  
TGAGGATCC

FIGURE 18K

Prostate 1

LTFFWLDRSVKAAAVLVHPQWVLTVKAAALLQERGVAYIKAALLLSIALSVNPLVCNGVLQGVK  
AAIMYSAHDTTVKAAAFLLTPKKLQCVNAMMNDQLMFLNAGLPSIPVHPVKAAALGTTTCYVGAAL  
LLWQPIPVNFLRPRSLQCVKAFLTLSTWIGVNALLYSLVHNLGAATLMSAMTNL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATTG  
ACATTTTTTTGGCTGGATAGATCGGTAAAGGCTGCAGCCGTGCTTGTTTCATCCCCAGTGGGTCT  
TGACCGTAAAGGCTGCCGCGCTGCTACAAGAAAGAGGGGTGCGATACATCAAAGCTGCTCTC  
CTCTTGAGTATTGCGCTAAGTGTAACCCGCTAGTTTGTAATGGGGTGTTACAAGGTGTGAAA  
GCGGCGATTATGTACAGTGCCACGACACTACCGTAAAAGCAGCCGCTTTCCTGACCCAAAA  
AAACTCCAATGCGTGAACGCAATGATGAATGATCAGCTGATGTTTTTAAACGCTGGCTTACCT  
TCTATACCGGTTTCATCCAGTCAAGGCCGCGGCATTGGGTACGACGTGTTATGTTGGAGCAGCG  
ATACTTCTTTGGCAGCCCATACAGTAAATTTTTTAAAGACCTAGATCCTTACAATGCGTCAAAG  
CATTCCTTACACTCTCAGTAACTTGGATCGGAGTCAATGCTCTGCTATATAGCCTCGTACACAA  
CTTGGGCGCGGCCACACTTATGAGTGCAATGACGAATTTAGCTAAGTTCGTGGCGGCCTGGAC  
TCTAAAGGCCGCAGCA

HIV-1043

MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGPGPWFEVNTPLVKLWYQGPGPGR  
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGPGPGEIYKRWIILGLNKIVRMYGPGPQGQM  
VHQAI SPRTLNGP GP GIKQFINMWQEV GKAMYGP GP GWAGIKQEF GIPYNPQGP GP GKTA VQMA  
VFIHNFKRGP GP GSPAIFQSSMTKILEP GP GPGEVNIVTDSQYALGI GP GP GHSNWRAMASDFNLPP  
GP GP GAETFYVDGAANRETKGP GP GGA VVIQD NSDIK VVP GP GP GFRKYTAFTIPSINNE

ATGGAGAAGGTGTACCTGGCCTGGGTTCAGCCCCACAAAGGCATCGGGGGAGGGCCCCGGACC  
TGGGCAGAAACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAG  
GTTGGGAGTTTGTGAACACACCACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCGGAT  
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCGGGCCAGGCCAG  
CACCTTCTGCAGCTTACAGTGTGGGGAATTAACACAGCTGCAGGGGCCGGGCCCCGGGGGGGA  
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC  
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGCCCAG  
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG  
GATGGGCAGGGATAAAACAGGAGTTTGAATCCCTTACAATCCCCAGGGTCCTGGGCCAGGT  
AAAACGGCAGTGCAGATGGCCGTGTTCAATCATAATTTTAAGCGGGGCCCTGGACCTGGCAGC  
CCAGCTATATTTCAAAGTTCGATGACCAAAATCTTGGAGCCCCGGCCAGGGCCGGGCGAAGT  
GAACATTGTACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCGGACCAGGGCATTCCAA  
TTGGCGCGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAACTTT  
CTATGTGGACGGCGCTGCAACAGGGAGACTAAGGGACCCGGACCCGGCGCGCTGTAGTCA  
TTCAGGACAACCTCAGACATCAAGGTGGTTCCTCGGTCCAGGCCCGGGTTCAGAAAGTATACCG  
CCTTCACTATTCCGTCCATCAACAATGAGTGA

FIGURE 18L

HIV-1043 PADRE

MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGPGPGWEFVNTPLVLWYQGP GPGYR  
KILRQRKIDRLIDGPGPGHLLQLTVWGIKQLQGP GPGGEIYKRWIILGLNKIVRMYGPGPGQGM  
VHQAI SPRTLNGPGPGIKQFINMWQEVGKAMYGPGPGWAGIKQEF GIPYNPQGP GPGKTA VQMA  
VFIHNFKRGP GPGSPAIFQSSMTKILEP GPGPGEVNIVTDSQYALGHGPGPGHSNWRAMASDFNLPP  
GPGPGAETFYVDGAANRETKGPGPGGAVVIQDNSDIKVVP GPGPGFRKYTAFTIPSINNEGPGPGA  
KFVAAWTLKAAA

ATGGAGAAGGTGTACCTGGCCTGGGTTCAGCCCCACAAAGGCATCGGGGGAGGGCCCCGGACC  
TGGGCAGAAACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAG  
GTTGGGAGTTTGTGAACACACCACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCCGAT  
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCCGGGCCAGGCCAG  
CACCTTCTGCAGCTTACAGTGTGGGAATTAAACAGCTGCAGGGGCCGGGCCCGGGGGGA  
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC  
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGGCCAG  
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG  
GATGGGCAGGGATAAAACAGGAGTTTGAATCCCTTACAATCCCCAGGGTCCTGGGCCAGGT  
AAAACGGCAGTGCAGATGGCCGTGTTTCATTTCATAATTTAAGCGGGGCCCTGGACCTGGCAGC  
CCAGCTATATTTCAAAGTTCGATGACCAAAATCTTGGAGCCCCGGCCCAGGGCCGGGCGAAGT  
GAACATTGTCACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCCGACCAGGGCATTCCAA  
TTGGCGCGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAACTTT  
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGGCGCTGTAGTCA  
TTCAGGACAACCTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCCGGGTTTCAAGAAAGTATACCG  
CCTTCACTATTCCGTCCATCAACAATGAGGGCCCCGGCCCAGGTGCCAAGTTCGTGGCTGCCT  
GGACCCTGAAGGCTGCCGCTTGA

HIV 75mer

EKVYLAWVPAHKGIGGPGPGQGQMVHQAI SPRTLNGPGPGSPAIFQSSMTKILEP GPGPGFRKYTA  
FTIPSINNE

GAGAAGGTGTACCTGGCCTGGGTGCCTGCCCACAAGGGAATCGGAGGACCTGGCCCTGGACA  
GGGACAGATGGTGCACCAGGCCATCAGCCCTAGGACCCTGAACGGACCTGGACCTGGAAGCC  
CTGCCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCGGACCTGGACCTGGATTCAAGGA  
AGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGTGA

FIGURE 18M

PfHTL

MQVQIQSLFLLLLWVPGSRGRHNWVNHAVPLAMKLIGPGPGKCNLYADSAWENVKNGPGPGKS-  
KYKLATSVLAGLLGPGPGQTNFKSLLRN LGVSEGP GPGSSVFNVVNSSIGLIMGPGPGVKNVIGPF  
MKAVCVEGPGPGMNYYGQENWYSLKKGP GPGGLAYKFVVPGAATPYGP GPGPDSIQDSLKESR  
KLNGPGPGLLIFHINGKIIKNSEGP GPGAGLLGNVSTVLLGGVGP GPGKYKIAGGIAGGLALLGPGP  
GMRKLAILSVSSFLFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGATCCAGA  
GGAAGGCACAACCTGGGTGAATCATGCTGTGCCCCTGGCTATGAAGCTGATCGGCCCTGGACC  
AGGGAAATGCAACCTCTACGCAGACAGCGCCTGGGAGAACGTCAAGAATGGCCCCGGACCTG  
GGAAATCCAAGTATAAGCTCGCTACCTCTGTGCTGGCAGGCCTGCTCGGACCAGGCCCCGGAC  
AGACAAATTTCAAAGCCTGCTCAGAAACCTGGGAGTGTCCGAGGGGCCTGGCCCAGGATCT  
AGCGTCTTTAATGTGGTCAACTCCTCTATTGGGCTCATCATGGGACCCGGACCTGGGGTGAAA  
AATGTCATTGGCCCATTCATGAAGGCCGTGTGTGTCGAAGGACCCGGGCCTGGCATGAACTAC  
TATGGAAAGCAAGAAAATTGGTACAGCCTGAAGAAAGGCCCTGGGCCAGGCGGACTGGCTTA  
CAAGTTTGTGGTCCCAGGGGCAGCCACTCCCTATGGGCCTGGGCCAGGCCCCGATTCCATCCA  
GGACTCTCTCAAAGAGAGCCGAAACTGAACGGACCCGGGCCTGGACTGCTCATTTTCCACAT  
CAATGGCAAAATTATCAAGAACAGCGAGGGACCTGGGCCAGGCGCCGACTGCTGGGGAACG  
TGTCCACCGTCCTGCTCGGCGGAGTGGGGCCCGGCCCTGGGAAGTACAAGATCGCTGGAGGG  
ATCGCAGGCGGACTGGCCCTCCTGGGCCCAGGACCAGGGATGCGCAAACTGGCTATTCTCTCT  
GTCTCCAGCTTTCTGTTTGTGTGA

FIGURE 18N

09394018-062701

Protein	Sequence	Restriction
HIV gag 386	VLAEAMSQV	HLA-A2
HIV gag 271	MTNNPPIPV	HLA-A2
HIV pol 774	MASDFNLPPV	HLA-A2
HIV pol 448	KLVGKLNWA	HLA-A2
HIV pol 163	LVGPTPVNI	HLA-A2
HIV pol 498	ILKEPVHGV	HLA-A2
HIV pol 879	KAACWWAGI	HLA-A2
HIV pol 132	KMIGGIGGFI	HLA-A2
HIV pol 772	RAMASDFNL	HLA-A2
HIV pol 183	TLNFPISPI	HLA-A2
HIV env 134	KLTPLCVTL	HLA-A2
HIV env 651	LLQLTVWGI	HLA-A2
HIV env 163	SLLNATDIAV	HLA-A2
HIV nef 221	LTFGWCFKL	HLA-A2
HIV vpr 59	AIIRILQQL	HLA-A2
HIV vpr 62	RILQQLLI	HLA-A2
HIV pol 929	QMAVFIHNFK	HLA-A3
HIV pol 722	KVYLAWVPAHK	HLA-A3
HIV pol 971	KIQNFRVYYR	HLA-A3
HIV pol 347	AIFQSSMTK	HLA-A3
HIV pol 98	VTIKIGGQLK	HLA-A3
HIV env 61	TTLFCASDAK	HLA-A3
HIV env 47	VTVYYGVPVWK	HLA-A3
HIV nef 100	QVPLRPMTYK	HLA-A3
HIV vif 7	VMIVWQVDR	HLA-A3
HIV gag 162	QMVHQAISPR	HLA-A3
HIV gag 545	YPLASLRSLF	HLA-B7
HIV gag 237	HPVHAGPIA	HLA-B7
HIV pol 186	FPISPIETV	HLA-B7
HIV pol 893	IPYNPQSQGVV	HLA-B7
HIV env 259	IPIHYCAPA	HLA-B7
HIV env 250	CPKVSFEPI	HLA-B7
HIV nef 94	FPVRPQVPL	HLA-B7
HIV rev 75	VPLQLPPL	HLA-B7
HIV pol 684	EVNIVTDSQY	HLA-A1
HIV gag 317	FRDYVDRFY	HLA-A1
HIV pol 368	VIYQYMDDL	HLA-A1
HIV pol 295	VTVLDVGDAY	HLA-A1
HIV pol 533	IYQEPFKNL	HLA-A24
HIV pol 244	PYNTPVFAI	HLA-A24
HIV pol 530	TYQIYQEPF	HLA-A24
HIV pol 597	YWQATWIPEW	HLA-A24
HIV env 681	IWGCSGKLI	HLA-A24
HIV env 671	RYLKDQQLL	HLA-A24

FIGURE 19A

Protein	Sequence	Restriction
HIV env 55	VWKEATTTLF	HLA-A24
HIV vpr 46	IYETYGDTW	HLA-A24
HIV vpr 14	PYNEWTLEL	HLA-A24
HIV gag 298	KRWIILGLNKIVRMY	HLA-DR
HIV pol 596	WEFVNTPLVWKLWYQ	HLA-DR
HIV pol 956	QKQITKIQNFRVYYR	HLA-DR
HIV pol 712	KVYLAWVPAHKGIGG	HLA-DR
HIV gag 294	GEIYKRWIILGLNKI	HLA-DR
HIV pol 711	EKVYLAWVPAHKGIG	HLA-DR
HIV env 729	QHLLQLTVWGIKQLQ	HLA-DR
HIV gag 171	QGQMVHQAI SPRTL N	HLA-DR
HIV pol 335	SPAIFQSSMTKILEP	HLA-DR
HIV env 566	IKQFINMWQEVGKAMY	HLA-DR
HIV pol 303	FRKYTAFTIPSINNE	HLA-DR
HIV pol 758	HSNWRAMASDFNLPP	HLA-DR
HIV pol 915	KTAVQMAVFIHNFKR	HLA-DR
HIV vpu 31	YRKILRQRKIDRLID	HLA-DR3
HIV pol 874	WAGIKQEF GIPYNPQ	HLA-DR3
HIV pol 674	EVNIVTDSQYALGII	HLA-DR3
HIV pol 619	AETFYVDGAANRETK	HLA-DR3
HIV pol 989	GAVVIQD NSDIKVVP	HLA-DR3
HCV NS4 1812	LLFNILGGWV	HLA-A2
HCV NS1/E2 728	FLLLADARV	HLA-A2
HCV NS4 1590	YLVAYQATV	HLA-A2
HCV NS5 2611	RLIVFPDLGV	HLA-A2
HCV CORE 132	DLMGYIPLV	HLA-A2
HCV NS4 1920	WMNRLIAFA	HLA-A2
HCV NS4 1666	VLVGGVLAA	HLA-A2
HCV NS4 1769	HMWNFISGI	HLA-A2
HCV NS4 1851	ILAGYGAGV	HLA-A2
HCV CORE 35	YLLPRRG PRL	HLA-A2
HCV NS1/E2 726	LLFLLLADA	HLA-A2
HCV LORF 1131	YLVTRHADV	HLA-A2
HCV CORE 51	KT SERSQPR	HLA-A3
HCV CORE 43	RLGVRATRK	HLA-A3
HCV ENV1 290	QLFTFSPRR	HLA-A3
HCV NS1/E2 632	RMVVG GVEHR	HLA-A3
HCV NS3 1396	LIFCHSKKK	HLA-A3
HCV NS4 1863	GVAGALVAFK	HLA-A3
HCV NS4 1864	VAGALVAFK	HLA-A3
HCV NS3 1262	LGFGAYMSK	HLA-A3
HCV Core 169	LPGCSFSIF	HLA-B7
HCV NS5 2922	LSAFSLHSY	HLA-A1
HCV NS3 1128	CTCGSSDLY	HLA-A1
HCV NS5 2180	LTDP SHITA	HLA-A1

FIGURE 19B

Protein	Sequence	Restriction
HCV Core 126	LTCGFADLMGY	HLA-A1
HCV NS3 1305	LADGGCSGGAY	HLA-A1
HCV NS4 1765	FWAKHMWNF	HLA-A24
HCV NS5 2875	RMILMTHFF	HLA-A24
HCV NS5 2639	VMGSSYGF	HLA-A24
HCV NS4 1765	FWAKHMWNFI	HLA-A24
P. falciparum SSP2-230	FMKAVCDEV	HLA-A2
P. falciparum EXP1-83	GLLGVVSTV	HLA-A2
P. falciparum CSP-7	ILSVSSFLV	HLA-A2
P. falciparum LSA1-94	QTNFKSLLR	HLA-A3
P. falciparum LSA1-105	GVSENIPLK	HLA-A3
P. falciparum SSP2-522	LLACAGLAYK	HLA-A3
P. falciparum SSP2-539	TPYAGEPAPF	HLA-B7
P. falciparum LSA1-1663	LPSENERGY	HLA-A1
P. falciparum EXP1-73	KYKLATSVL	HLA-A24
P. falciparum CSP-12	SFLFVEALF	HLA-A24
P. falciparum LSA1-10	YFILVNLI	HLA-A24
P. falciparum SSP2-14	FLIFFDLFLV	HLA-A2
P. falciparum EXP1-80	VLAGLLGVV	HLA-A2
P. falciparum EXP1-91	VLLGGVGLVL	HLA-A2
P. falciparum SSP2-523	LACAGLAYK	HLA-A3
P. falciparum EXP1-10	ALFFIIFNK	HLA-A3
P. falciparum LSA1-11	FILVNLLIFH	HLA-A3
P. falciparum SSP2-126	LPYGRTNL	HLA-B7
P. falciparum CSP-15	FVEALFQEY	HLA-A1
P. falciparum LSA1-1794	FQDEENIGIY	HLA-A1
P. falciparum LSA1-9	FYFILVNLL	HLA-A24
P. falciparum SSP2-8	KYLIVVFLI	HLA-A24
P. falciparum CSP-394	GLIMVLSFL	HLA-A2
P. falciparum EXP1-2	KILSVFFLA	HLA-A2
P. falciparum CSP-344	VTGNGIQVR	HLA-A3
P. falciparum LSA1-59	HVLSHNSYEK	HLA-A3
P. falciparum SSP2-207	PSDGKCNLY	HLA-A1
P. falciparum LSA1-1671	YYIPHQSSL	HLA-A24
P. falciparum LSA1-1876	KFIKSLFHIF	HLA-A24
P. falciparum SSP2-13	VFLIFFDLFL	HLA-A24
P. falciparum LSA1-1881	LFHIFDGDNEI	HLA-A24
P. falciparum CSP-55	YYGKQENWYSL	HLA-A24
P. falciparum LSA1-5	LYISFYFI	HLA-A24
P. falciparum CSP-2	MRKLAILSVSSFLV	HLA-DR
P. falciparum CSP-53	MNYYGKQENWYSLKK	HLA-DR
P. falciparum CSP-375	SSVFNVVNSSIGLIM	HLA-DR
P. falciparum SSP2-61	RHNWVNHAVPLAMKLI	HLA-DR
P. falciparum SSP2-165	PDSIQDSLKESRKLN	HLA-DR3
P. falciparum SSP2-211	KCNLYADSAWENVKN	HLA-DR3

FIGURE 19C

Protein	Sequence	Restriction
P. falciparum SSP2-223	VKNVIGPFMKAVCVE	HLA-DR
P. falciparum SSP2-509	KYKIAGGIAGGLALL	HLA-DR
P. falciparum SSP2-527	GLAYKFVVPGAATPY	HLA-DR
P. falciparum EXP1-71	KSKYKLATSVLAGLL	HLA-DR
P. falciparum EXP1-82	AGLLGNVSTVLLGGV	HLA-DR
P. falciparum LSA1-16	LLIFHINGKIIKNSE	HLA-DR
P. falciparum LSA1-94	QTNFKSLLRN LGVSE	HLA-DR
HBV core 18	FLPSDFFPSV	HLA-A2
HBV env 183	FLLTRILTI	HLA-A2
HBV env 335	WLSLLVPFV	HLA-A2
HBV pol 455	GLSRYVARL	HLA-A2
HBV pol 538	YMDDVVLGV	HLA-A2/A1
HBV pol 773	ILRGTSFVYV	HLA-A2
HBV pol 562	FLLSLGIHL	HLA-A2
HBV pol 642	ALMPLYACI	HLA-A2
HBV env 338	GLSPTVWLSV	HLA-A2
HBV core 141	STLPETTVVRR	HLA-A3
HBV pol 149	HTLWKAGILYK	HLA-A3/A1
HBV pol 150	TLWKAGILYK	HLA-A3
HBV pol 388	LVVDFSQFSR	HLA-A3
HBV pol 47	NVSIPWTHK	HLA-A3
HBV pol 531	SAICSVVRR	HLA-A3
HBV pol 629	KVGNF TGLY	HLA-A3/A1
HBV pol 665	QAFTFSPTYK	HLA-A3
HBV core 19	LPSDFFPSV	HLA-B7
HBV env 313	IPIPSSWAF	HLA-B7
HBV pol 354	TPARVTGGVF	HLA-B7
TB	RMSRVTTFTV	HLA-A2
TB	ALVLLMLPVV	HLA-A2
TB	LMIGTAAAVV	HLA-A2
TB	ALVLLMLPV	HLA-A2
TB	GLMTAVYLV	HLA-A2
TB	MALLRLPV	HLA-A2
TB	RMFAANLGV	HLA-A2
TB	SLYFGGICV	HLA-A2
TB	RLPLVLPV	HLA-A2
TB	RLMIGTAAA	HLA-A2
TB	FVVALIPLV	HLA-A2
TB	MTYAAPLFV	HLA-A2
TB	AMALLRLPLV	HLA-A2
p53 139	KLCPVQLWV	HLA-A2
CEA 687	ATVGIMIGV	HLA-A2
CEA 691	IMIGHLVGV	HLA-A2
Her2/neu 689	RLLQETELV	HLA-A2
MAGE3 112	KVAEIVHFL	HLA-A2

FIGURE 19D



Protein	Sequence	Restriction
Her2/neu 369	KVFGSLAFV	HLA-A2
CEA 605	YLSGANLNV	HLA-A2
MAGE2 157	YLQLVFGIEV	HLA-A2
Her2/neu 665	VVLGVVFGI	HLA-A2
p53 149	SMPPPGTRV	HLA-A2
PAP.21.T2	LTFFWLDRSV	HLA-A2
PAP.112	TLMSAMTNL	HLA-A2
PAP.284	IMYSAHDTTV	HLA-A2
PSM.288.V10	GLPSIPVHPV	HLA-A2
PSM.441	LLQERGVAYI	HLA-A2
PSM.469L2	LLYSLVHNL	HLA-A2
PSM.663	MMNDQLMFL	HLA-A2
PSA.3.V11	FLTLSVTWIGV	HLA-A2
PSA.143.V8	ALGTTCYV	HLA-A2
PSA.161	FLTPKKLQCV	HLA-A2
HuK2.4.L2	LLLSIALSV	HLA-A2
HuK2.53.V11	VLVHPQWVLTV	HLA-A2
HuK2.165	FLRPRSLQCV	HLA-A2
HuK2.216.V11	PLVCNGVLQGV	HLA-A2

FIGURE 19E